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(54) Title: BIALLELIC MARKERS (57) Abstract The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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BIALLELIC MARKERS

RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., W0 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include β -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a

5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays

10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for

15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to

20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with

15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same

20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site

25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include

30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

II. Analysis of Polymorphisms

A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

20 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

3. Allele-Specific Primers

5 An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in
10 conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows
15 a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of
20 the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

4. Direct-Sequencing

The direct analysis of the sequence of polymorphisms of
25 the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,
30 1988)).

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5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

- $p(\text{ID})$ is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies x and y , the probability of each genotype in a diploid organism is (see WO 95/12607):
- 10 Homozygote: $p(\text{AA}) = x^2$
 Homozygote: $p(\text{BB}) = y^2 = (1-x)^2$
 Single Heterozygote: $p(\text{AB}) = p(\text{BA}) = xy = x(1-x)$
 Both Heterozygotes: $p(\text{AB}+\text{BA}) = 2xy = 2x(1-x)$

- The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:
- 15 $p(\text{ID}) = (x^2)^2 + (2xy)^2 + (y^2)^2$.

- These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity $p(\text{ID})$ for a 3-allele system where the alleles have the frequencies in the population of x , y and z , respectively, is equal to the sum of the squares of the genotype frequencies:
- 20 $p(\text{ID}) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + y^4 + z^4$

In a locus of n alleles, the appropriate binomial expansion is used to calculate $p(\text{ID})$ and $p(\text{exc})$.

- The cumulative probability of identity ($\text{cum } p(\text{ID})$) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.
- 30

$$\text{cum } p(\text{ID}) = p(\text{ID1})p(\text{ID2})p(\text{ID3})\dots p(\text{IDn})$$

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The cumulative probability of non-identity for n loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5 If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10 B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15 Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20 If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child
25 attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30 The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3})\dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of
5 individuals who have been tested for the presence or
absence of a phenotypic trait of interest and for
polymorphic markers sets. To perform such analysis, the
presence or absence of a set of polymorphisms (i.e. a
polymorphic set) is determined for a set of the
10 individuals, some of whom exhibit a particular trait, and
some of which exhibit lack of the trait. The alleles of
each polymorphism of the set are then reviewed to determine
whether the presence or absence of a particular allele is
associated with the trait of interest. Correlation can be
15 performed by standard statistical methods such as a χ^2 -
squared test and statistically significant correlations
between polymorphic form(s) and phenotypic characteristics
are noted. For example, it might be found that the
presence of allele A1 at polymorphism A correlates with
20 heart disease. As a further example, it might be found
that the combined presence of allele A1 at polymorphism A
and allele B1 at polymorphism B correlates with increased
milk production of a farm animal.

Such correlations can be exploited in several ways. In
25 the case of a strong correlation between a set of one or
more polymorphic forms and a disease for which treatment is
available, detection of the polymorphic form set in a human
or animal patient may justify immediate administration of
treatment, or at least the institution of regular
30 monitoring of the patient. Detection of a polymorphic form
correlated with serious disease in a couple contemplating a
family may also be valuable to the couple in their
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where Y_{ijkpn} is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record; μ is an overall mean; YS_i is the effect common to all cows calving in year-season; X_k is the effect common to cows in either the high or average selection line; β_1 to β_{17} are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms; PE_n is permanent environmental effect common to all records of cow n ; a_n is effect of animal n and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and e_p is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction θ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions (θ), ranging from $\theta = 0.0$ (coincident loci) to $\theta = 0.50$ (unlinked). Thus, the likelihood at a given value of θ is: probability of data if loci linked at θ to probability of data if loci unlinked. The computed likelihoods are usually expressed as the \log_{10} of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of θ (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of θ at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of θ) than the possibility that the two loci are unlinked. By convention, a combined lod score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

IV. Modified Polypeptides and Gene Sequences

The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component) except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or
5 other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate
10 promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host
15 sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include
20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing
30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, 5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is 10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene 15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating 20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide-fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference
25 sequences of the fragments shown in the Table, column 1. The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTAACTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACACATGCCAGTTGGGAAGTCT GAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAAGAGAGAGTGGAGACCAATCTTTATTT GTACTGGCCAAATACTGAATAACAGTTGAAGGAAAGACATTTGGAAAAAGCTTTTGAGGATAATGT TACTAGACTTTATGCCATGGTGCTTTTC/TAGTTTAAATGCTGTCTCTGTCCAG
WI-7070	226	C	T	---	---	AAGCCATTGACGTAACATCTCAGAGGTTATTTGCATGGATTGACTCCTGGGACAAAAGGAC/GC/JAA AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTTT GATAATACATAAAGCCCTAGGATTTAGATACAATCTTGAAGAACTGAGACAGATAATCTGAAATT AAATGAGGTAAAGTTTCAGGCACTCA
WI-10744	61	G	C	---	---	GGGCAAAATTACCAGCAAAAAGTCAAAATACCAGCATCAAAGTCAGGTGCAAGAGGTAGAGAACAA TTACAGTAACATATGTCAATCTTTTGTATATTAGTATTATCTGCCCAATGCCTAGAAATG/C/TJAGTG GGTCCCTAAATAGTATTAGTCCCTTTTCTCTCTCTCTCACTCTGAAATTTTATATACTTAA GGGATTAGTTACCACCAAAATGTGTATGATCAATTTGATCTTACTGAA
WI-9975	126	C	T	---	---	GCTAGGTTTGTCTGTTGGCTGCTTCACTAGACTTGAGATGACTTACAGTAATCCCTATGTT GATGTAACATAGCTAGACCTTCCCTTCTCCGCAATCCAGCTCCAGGTTTTCAGAAAGTATGCCACAC TCAACCTTCTCTCCAGTTCACTCTGATTAATTTCTCCCATATTAATTCAAAGGAGTGGACAGGT CCCTGGCTGAAAAGAAATAAAGAGATCCCAAGTGCTGGGG/GT/JCTT
WI-8010	247	G	T	---	---	GCCGGGCTATCTTTTAACTTTAACTTGATCTTTGGTGTCTTCCATCCTAGGATTCTGCCTTATAAT CTTTGTCTGTGTG/GC/JATTACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGGCCAATCTTCAGGCTCTTTGAAATTTCTCTGCTATTGAGGACATTCACACTTCTACTTAA TCTCGACTCTATAACAACCTCCACAGAA
WI-5222b	85	G	C	---	---	GCCGGGCTATCTTTTAACTTTAACTTGATCTTTGGTGTCTTCCATCCTAGGATTCTGCCTTAT AATCTTTGTCTGTGTGATTAACCTGATCTACTTTTGATACACAAGGCTGATGGCTCACAATGT AGTAGGCCAATCTTCAGGCTCTTTGAAATTTCTCTGCTATTGAGGACATTCACACTTCTACTTAA TCTCGACTCTATAACAACCTCCACAGAA
WI-5222	52	G	C	---	---	TATGCATTCACAAAAGCGATATAATTTAAAAGTTTTTTCATTAGAAATAAATGTATAAAAATAA ATATGTTATTATAGGCATTTTACTAACTATAGTCTCTTGGGAAGGAACACCCAAACCAATACTT ATAAAGTACATGTAATTTATAGTAACATATTTACTATATACATATGGAATAATCATATTTCTCACA GAAGAGCTGAACAGACATTCACCAGGATACGACTGTGGAG/C/JAAGCTGCTG
WI-8007	242	C	A	---	---	TCAGTTGCAAAAATTGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGATGTGTTTTGTTAG TCTATATTCACACATATGAGTGAAATTTCT/JTGGGCGCATGGGAAATACATCTTTATGAGACATGGA ACTGCTCACCACATCATAGTATCCATTTAAACAGACCAACAATGTATAAGAAATTCCTTTGTTTTAC ATGCTTCCAAATCTGATTTTGTATGACTATTGTATGCACAGTTGGATCAAC
WI-9823	97	C	T	---	---	

WI-9551b	105 A T ---	---	TCTACATCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAATTCCTTTCCCT ACTTGCTCCTCATGTACAATTTTCTGCTGCTCCTCA/ATGGGGCAGCTTGAAGCCCTCCCTTTTAGAC ACCTCTACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCTCTG CTTTAAACCTGTAAATGGTATATTAATCCTTGGTGTTGAATGTCCTC
WI-9651	139 T C ---	---	TCTACATCTATGGACAACCTCCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAATTCCTTTCCCT ACTTGCTCCTCATGTACAATTTTCTGCTGCTCCTCAAGGGGAGCTTGAAGCCCTCCTTTAGACACCT CT/CACAGGTACAGCCGACCATGCCCTACCTCCATGGCACTGCCAGGGACCCCTTATAGGCTCTGT CTTTAAACCTGTAAATGGTATATTAATCCTTGGTGTTGAATGTCCTC
WI-7676b	309 A C ---	---	GTGACCTTCCTGCAGGTGGAGATGGACATCCTTGTCTGCTGGGACCTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAGGTAGATGGGAGGGTCTGTGTGAAGGG GCGGCTCTCTTGGTGCCTGCTGGTTCAGGGGAGGAGCGTGTGGACTGCAGCTTCTGCTGGTGC TCCCCCGTCTCCTGGAGGAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139 C T ---	---	GTGACCTTCCTGCAGGTGGAGATGGACATCCTTGTCTGCTGGGACCTTGGCCCTGCTATTTATTTTG TATTTATGCTTAATCTCTCCACTGATGCATCCTCCAAGGTAGATGGGAGGGTCTGTGTGAAGGG GC/ATGGCTCTCTTGGTGCCTGCTGGTTCAGGGGAGGAGCGTGTGGACTGCAGCTTCTGCTG GTGCTCCCCCGTCTCCTGGAGGAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105 G A ---	---	CATTATCTTGCTTGGGCTGTTCATTCACTTTCCTCTCTCCAATGAAGAGGATATTTAAGCATCAAT CATCTGGCCCTTTTGGAGTTTGAATAATTTTGTG/ATGACTCCTATGCACATGATAAATTTGTTA TGCTTGCTCTTATCTTATCTTTGTTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAAGGGA TCACCCCTTTTGGCTCTACAACCTTATAGATAATTTAATATCTTT
WI-9986	42 T C ---	---	TTGGTGTGAACCTCAGAAATAGGGAAAATAGACAATTTGAAT/A,CJGTACCCAGGAAACAGAG CCCTGCACTTGACTCCAAAGGAGTTCTATATCTGGCTGTTCCAGACTTTATGTATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTACAAGAACATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACTTATTGCAATT
WI-7041	174 C A ---	---	GTCTATTGCAGGAGAAAGTCCCTTGGCACTCCCACTCTCATCAGGCAAGTGAGGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCTCAGAGAGCTGAAAGGGTCCCTCGGCTCTTTATTT CAGGGCTTTCATGCGCTCTATTCCCCCTCTGCTCTC/ATCCACCTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAAACAAGCTCAITTTGTACAGTGTCTGTTCATGTAAATA
WI-7224	134 T C ---	---	ATAAACCTTGTGTATGTATCACCACCTCACTAATTAATCAACTATGTGCTATCAGATATCCTCTCT ACCCCTCAGCTTATTTGAAGAAAATCCTAAACATCAATACTTTTCATCCATAAAATGTCAGCATTT /CJATTAATAAACCAATAACTTTTAAAGAAAACATAAGGACACATTTTCAAATTAATAAAATAAAG GCATTTTAAGGATGGCCTGTGATTATCTTGGGAAGCAGAGTGATTCATGCTAG

WI-10826	132 A C ---	---	---	TCTTATTTGCATTTCACAGTAGCCCCATGAAGTAGGTAGGTATACCAGCCTCTATTTTAAACATGAGAAGAT GGAGGCCCTTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTCTTAATAAGCAAAGACCTGCA[VC JCCCTGGCTTCTGACTCCAAAGCTTATCCCTTCTCATGCTGTTGCTGTCAGCCAGGACCCCATGGCA GAAAGCCAGCCTCTCCATCCCCAC
TIGR- A004S25	145 G A ---	---	---	AGATCTGCCATTAGTATTTATCTTTGAAGATACITTTGGAGATTCAITTTCTTGAGTGGCACTGCA GCTCATTGAGTGAACACITTTGGGGTATAGAAATGGAATGGAGAGTTTCAAACAGCTTTGCTGAAAC TGTACTTTGG[G/A]CTCCAGACTTCACTGTCTTAGGCATTGAAACCATCACCTGGTTTGCAITCTTG ATGACTGAGGTTAACTTAAATGACITGAGGTTAACTTAAAC
WI-1021	24 A T ---	---	---	AAACACACAGAAATCATCAAGCAC[A/T]ATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAAGTAACTCTGAAATAGTAGGATAGTATTATCATTTCTGTAAATAGATTCACTCTCAGCAAT TGGTCTGTTTTCATTTCTATGGAACCTCTCCGTAAGTAAATTTTCAITCTATGGAACCTCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121 G T ---	---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATAGAACACITTTGAATGGTCTTGTC TTTCAATAAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGGCCTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGATTAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAACCAAGAGAGAACTTGAT
WI-4719b	107 T G ---	---	---	TTCAITTTCCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTTGGGTGTAGCGGATT ATGCTGACGCCATGGGTGTTTCAATAGTGACTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTT CTGTGAGGGGCATGTAATTGTATTTCATTCAACAATTTCTGCTATGCTTCTCAGATTGCAGAAATCAC TGCTCAAAATCCCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70 G A ---	---	---	TTCAITTTCCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTTGGGTGTAGCGGATT AT[G/A]CTGACGCCATGGGTGTTTCAATAGTGACTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTT CTGTGAGGGGCATGTAATTGTATTTCATTCAACAATTTCTGCTATGCTTCTCAGATTGCAGAAATCAC TGCTCAAAATCCCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216 G C ---	---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCTGCCAGCAAGATTCTTACCTTACCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTTCTCTCTGACACTGCCAAGT TAAAGAAACCCCTGCTTCTGAGAGGGAGGGCCAGACAGGGAATTCAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGGACAGGGTTCCAACTTT
WI-9484	178 G A ---	---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCTGCCAGCAAGATTCTTACCTTACCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTTCTCTCTGACACTGCCAAGT TAAAGAAACCCCTGCTTCTGAGAGGGAGGGCCAGACAGG[G/A]AGGAAATTCAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACAGGGTTCCAACTTT

WI-7330	207	C T	---	---	AGGATGGAAGGAGACACGGGGCAGGGGAGAACTCTCTCTGCTAAATCGATAGGAGTCAGTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTCTTTAATTTGGGCATATAGGTTT GTGACACAAGAAAGTCATACTTTGGTGGCTAAGTTTACTAAGGAAATAACTGAAAGATTAAG TGAGAG[C/T]TGAAAAGAGAAATGATAATGCTTCCAACTGTAGCTGTCACAG
WI-9443	211	G A	---	---	TAAAAACAGTTCAGGTTGGTGAAGCAGAAAGGGATGTATTACAAATTTAAATGAATCAGTCACCT GCACAATTAATCTCTTGGCATACAAACTGGGTTTAAATGGCAATGATGACATCATAGCATGA CCAACACTCATGAAGGCAGTCTAGAGTCCATCACGCTACACCTGAGGGGAAGGCACTGCACCCA CTGACGAGAC[G/A]CAGAGACCTTGGACTACAGATGACACCATGCCACTT
WI-7166	59	C T	---	---	TCTCTCAAAAGAGAAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA[C/T]GGAT CATCAACAAGATTCCTTGTGCAAAATATTTGACTATTCTGTATCTTTCATCTTGACTAAATTCGTG ATTTCAAGCAGCATCTCTGGTTTAACTTGTTCGTGAACAAATGTCGAAAAGAGTCTTCCAAT TAATGCTTTTATATCTAGGCTACCTGTTGGTTAGATTCAAGGCCCGAG
WI-7259b	189	T C	---	---	GCTCTTCCCAGGAAGCGGGTCTTGGCTGGAACCTTCCAGAGAGGAGCGGGAGCAATTTAGCC CCACCCTGCTCCCATCTGCCCTGCAACAGCTGCAGGCTGCTCTCTCTGAGTTCTCTGGCT GGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAGT[C/T]GGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCCTGGAGCTC
WI-7259	188	G T	---	---	GCTCTTCCCAGGAAGCGGGTCTTGGCTGGAACCTTCCAGAGAGGAGCGGGAGCAATTTAGCC CCACCCTGCTCCCATCTGCCCTGCAACAGCTGCAGGCTGCTCTCTCTGAGTTCTCTGGCT GGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAG[C/C,T]TGGGGGAGCA GAGCAGCAGGTGGACAGGTGTTTGCAGGGGCCCAACTTCCCCTGGAGC
WI-7322	275	A G	---	---	GTACTTTAGGCTGTGAGGGTGGCATTTAGTGGTGACCTTGACCCAGGGTTTCTAACAGATGAC CCTGTGAATCATAATTTAACTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCCTATAG GCCATAAAGTGCCTAAGCACTCAGGCTCCCACTCCCACTCAACCCCTTTGACCAGAGAAAGCACTC TGGTTCTCTATCCCCTTGTACATAGAGAGTTTGTATGGGGCTCTGGCTG
WI-7685	46	T C	---	---	TCAGTTCTAGTCTCTCTGGGGCCACACAGAACTCTTTTGGGCTG[C/T]TTTCTCCCTCTGGATCA AAGTAGGACGAGGACCATGGGACCAAGTCTTGGAGCTGAGCCTCTACCTGTACTCTTCCGAAAAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCCTGTATCTCCATGGCTTCTCTCCCTCTGCGGACTC CTGGGTTGAGCTGTTGCCTCAGTCCCCCAACAGATGCTTTCTGCTC
WI-563	87	G A	---	---	TGTGACCAATTTGTTATTTTAGAGGGTTTAAACAATGGCCTGACTATCACCTGATGGTGGCCAGAAATTC CTGGGGGAGGGCTCCCT[G/A]CCCCTGATCATGTCTACCTAAGTGCCTGACTCTAACAAATACTACTCC TGTGGTATGGGGATCCTAAGCCAAAAAGCTGAAATGAACATGTTCTAGCACTACAGAAATCCACT GCCCTCAGTAAAGGCAATTTTAAATCTCTTTGGATAACCCAGGGGCACAT

WI-931c	191 C A ---	---	GACCAGGGCACCAGAAAGCCACGGAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATCTGCTGTGTCAAAATGATCCTTCT GTTGCTGCACCTGTCTATTACTGTGTATGGATTATATTATGTCCTCAAAAAGCC[C]A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTA]G]TCCCTCACCACACCTTCCAGTGCTTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACCTGTCTATTACTGTGTATGGATTATATTATGTCCTCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31 A G ---	---	GACCAGGGCACCAGAAAGCCACGGAGCCAC]A]G]GCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTTCTCTCCCTCCCTATCCCTCACCACACCTTCCAGTGCTTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACCTGTCTATTACTGTGTATGGATTATATTATGTCCTCAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91 C T ---	---	GGATGACTTACCCCAATAGCAGGGTGGGTACATTCATGGGTAAACACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGG[C]T]ACCTACTTAGAGCAGTGGAGTACCCCTGAGTACGACCCOC TTAGCAGCAGAAATACAAGAAATCTTGGGACCTGTACTCTGATACAAAATAAGGACATGGGTACGC CTGAGCCACTCTTAAACCAATGAACCATCACCATTTAAATAACGTTGCCCCCC
WI-10870	103 G A ---	---	GGATGACTTACCCCAATAGCAGGGTGGGTACATTCATGGGTAAACACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGACACCTACTTAGA]G]A]G]AGTGGAGTACCCCTGAGTACGACCCCC TTAGCAGCAGAAATACAAGAAATCTTGGGACCTGTACTCTGATACAAAATAAGGACATGGGTACGC CTGAGCCACTCTTAAACCAATGAACCATCACCATTTAAATAACGTTGCCCCCC
WI-7719b	281 T C ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTTGGTCTGGCCAGTCTACAATGTCCCAATATCAAGGACACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTTGCCCATGTATAATCCTCAGTGAATTTCAAGCTAAAGCAA
WI-7719	163 A G ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGGCATTTGGTCTGGCCAGTCTACAATGTCCCAATATCAAGGACACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC]A]G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTTGCCCATGTATAATCCTCAGTGAATTTCAAGCTAAA
WI-10396	72 C A ---	---	GCCTGGAGTATATCTAACTGTGGCCCTCCACTTTCTTCTGAAACATTTGCTATCAACTGGGAA GAGT[C]A]TGTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTTGTTTCTTTTGTGA TGCCATTTGAGGGATTGATGTTTCTTAACTATGAAGTACTTGGCTGTCTCTCTCCATTTGCTGTTACGG TTAACAGCCACCATTTGTAACACTTTGT

WI-10673	94 C G ---	---	TCCCTTTATGCACCCCAAGAGATATTTATTAAACACCAATTACGTAGCAGGCCATGGCTCATGGGAOC CACCCCGGTGGCACTCATGGAGGGGCG/GJTGAGGTTGGAACATATGCAGTGTGCTCCGGCCACACA TCCTGTGGGCCCCCTACCTGCCCAATTCATCCTGCCAATAAATCCTGCTCTTATTGTTTCATCCTG GAGAAITGAAGGGAGGTCAGTTGTTTGCAATGATTGTGAGAGAACCT
WI-7842	57 T C ---	---	CACAGCCATGCCCTTGAGAGCGGCCACAGATGCTGAATCCCTATCCCCATTCTGT/CJGTATGAG TCCCAITTTGCCTTGCAATTAGCATTTCTCTCCCCAAAAAGAAATGTGCTATGAAGCTTTCTTTCCCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGCTTAGTACCAGAGCTAGTTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTACAGCTCCCTTATA
WI-7721	145 A C ---	---	CTGCCTCATCAGCCCACTGGAGTCCACACTTGAATTTGGGCAGCTACCACGGGCTGCGCATGCTCTGG AGGACAAAGGGGGCCACATCCCCACCCAGCTGTACCCAGCCGGGCGAGGTGCAGCCCTTCCTCCOC TGCTCTGCG/CJGTGACTCTCTTTGAGGTCCCTGTATGTCTACCTCTGACTTCTGTGGTCCCTCTG TGCTGCTCTCATCCATTCCTCTTACTGGGSCCTGGGGCTCTAGCCCAA
WI-4767b	173 C A ---	---	TTCCAGTCTGTTTATCCTTTTATCCTTTTATGTCAAAAAGATGCTCTTAGACTGAAATTCATAAGAGTTCCT CAGGTCTGGGTAATCCTAGATCTTCCCTATATCCATTGAGTGTGAGTGGAGAGAGGGTATGTTT CTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACA/CJAATCACTAAGGAATTCACACTAAGA CTCCTCTAACCCAGAGATTTTAAACCT
WI-4767	50 A G ---	---	TTCCAGTCTGTTTATCCTTTTATGTCAAAAAGATGCTCTTAGACTGA/CJGATTCATAAAGAGT CCTCAGGTCTGGTAATCCTAGATCTTCCCTATATCCATTGAGTGTGAGTGGAGAGAGGGTATG TTCTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCACACTAAGAC TCCCTAACCCAGAGATTTTAAACCT
WI-7718f	222 C T ---	---	ATTGCACTGAAGTTTGTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAAGTTCACTACATGTTCTGGGGCCCCGGAGATAGTG ACTTTGCAGATGGAAGAGGTGAAAAATGAAGAGGAAGCTGTGTTGAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA/CJTCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718e	60 T C ---	---	ATTGCACTGAAGTTTGTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGA/CJGCAA GGATTACAGAACTGATGCCAAGGGGCTGAGTGAAGTTCACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAAATGAAGAGGAAGCTGTGTTGAACAGAAAAATAAGTCA AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718d	31 G A ---	---	ATTGCACTGAAGTTTGTGAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGGCTGAGTGAAGTTCACTACATGTTCTGGGGCCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAAAATGAAGAGGAAGCTGTGTTGAACAGAAAAATAAGTCA AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	248	A G ---	91 C G ---	---	ATTGCACTGAAGTTTGTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGG[C/G]TGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTCAGATGGAAGAGGTGAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718b	248	A G ---		---	ATTGCACTGAAGTTTGTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTCAGATGGAAGAGGTGAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAGJAT
WI-7718a	42	A T ---	C	---	ATTGCACTGAAGTTTGTGAAATACCTTTGTAGTTACTCAAGC[A/C]TGTTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTCAGATGGAAGAGGTGAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTA
WI-7227d	99	G C ---		---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTTCATCTTTCAGACAAGCTTTAGJAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGTGTATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTCAACCAGCGACTAATG
WI-7227c	291	G A ---		---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT GGTTAGTATCTGTGTTCCGGTGGTGTATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACAGTG TTATTATGGGAAAGGAAATGGCATTGCTGCTTCAACCAGCGACTAATGCAAT
WI-7227b	93	G T ---		---	AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGCTTC CGTGGACCAATTTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGTGTATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTCAACCAGCGACTAATG
WI-7227a	24	A G ---		---	AGGGAATTGTGTTGCTCCTGGAGG[A/G]AGCCAGGCATCATTAAACAAGCCAGTAGGTCACCTGGC TTCCGTGGACCAATTTCATCTTTCAGACAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTGGTTAGTATCTGTGTTCCGGTGGTGTATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTCAACCAGCGACTAATG
WI-7310b	234	A C ---		---	CCACAATGCCTCCTCCACGATGTCAGGACTCCTGCTGCTGAGGTGGGAGACAAGGAACCTCCG AAGAGGAAGCAAGAAAGCCGCTACTGCTATGTTGATCCTTCATCGAACAACTGATGCGAAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACGTAGGCCAACACACTGTAAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA[A/C]ATGATCTTGAGATTTC

WI-7310a	64 T A ---	---	---	CCACAATGCCCTCTCCACGATGTCAAGGACTCCTGCTGCTCCTGGAGGTGGGAGACAAGGAACCTT/A JCGAAGAGAGGAAGCAAGAACCGCTACTGTCTATGTTGTGATCCTTCATCGAACAACTGATCGGAA AACTTGAATCTGTTACTGAATGAGGAGAGAGACATGTCTATTGAACCTGAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	---	CCAGCAACACCTACACCTTGTACCTGCCTGGGACTCCTATGATGGCCTGCTGGTTGATAATAATCA GATCATGCCCAAGACGGGCTCCTGATAATCGTCTTGGGCATGATTGCAATGGAGGCAATCGGTCC CTGAGGAGAAATCTGGGAGAGCTG[A/G]GTGTGATGAAGGTGATGTTGGGAGGGAGCACAGTGT CTGTGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAAACTA
WI-7878a	51 C G ---	---	---	CCAGCAACACCTACACCTTGTACCTGCCTGGGACTCCTATGATGGCCTGCTGGTTGATAATAA TCAGATCATGCCCAAGACGGGCTCCTGATAATCGTCTTGGGCATGATTGCAATGGAGGCAATGTC GTCCCTGAGGAGAAAAATCTGGGAGAGCTGAGTGTGATGAAGGTGATGTTGGGAGGGAGCACAGTG TCTGTGGGAGGCCAGGAAGCTGCTACCCCAAGATTGGTGCAGGAAAACTA
WI-7381c	213 C T ---	---	---	CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTTTCTTCTACC AGCCCTGCAAGTTTCTCATGAGCGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAGATC AGATGTGCCAAGGGAAGGAGCTGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAGACA AAACGGCTCCTGCTGCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	---	CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTGCTTCTTCTCT ACAGCCCTGCAAGTTTCTCATGAGCGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAG ATCAGATGTGGCCAAAGGGAAGGAGCTGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	---	CTCCACATTCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGGAATCCCTGCTTCTTCTCT ACAGCCCTGCAAGTTTCTCATGAGCGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGGTGAG ATCAGATGTGGCCAAAGGGAAGGAGCTGTTCCAGAGAAATTCACAAAGTTCCCTCTGTACAGAG ACAAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	---	AAATTGCTCTATTGGACCCCTCATATTAAATAAGAGCAATGAGAGCGGGAATTTGAATCTCTC AGGTACTGACTGTGGGACCAGACAAG[G/A]GATGTAGATTGTACATTCATCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGAGGTTTGTCCC
WI-1017a	92 G A ---	---	---	AAATTGCTCTATTGGACCCCTCATATTAAATAAGAGCAATGAGAGCGGGAATTTGAATCTCTC AGGTACTGACTGTGGGACCAGACAAG[G/A]GGATGTAGATTGTACATTCATCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTTCAAAATAAGGAGTGTGAGGTTTGTCCC

WI-1795b	130 T C ---			GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTTCTCCAGACTCTCAGGATTA AATTGTATGCATGTGAACAACCTGAGGTACTTTAGATCTCAGTGCCTTGCGAGAAAGAAAGT/C/C GTCTACCATTTTCACCAAATTTCTGAGTACAATTTAAGTATCTCTTGTTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-1795a	47 T C ---			GAAGCAACCAGAAAGTATCTTTATCCCATCTAGATTATGTCTGGGTT/C/CCTCCAGACTCTCAGGA TTAAATTGTATGCATGTGAACAACCTGAGGTACTTTAGATCTCAGTGCCTTGCGAGAAAGAAAGT GTCTACCATTTTCACCAAATTTCTGAGTACAATTTAAGTATCTCTTGTTATCTCCCTAGGAGTCTAA AGTGAGCTGGGGAAGGCAGGATTT
WI-10616d	136 G A ---			CACACAAATTTGCAACACTTCAAAGTGAACGCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCCATACGTAGGTCTGGTCTCTCTATCACAATTGCCA C/GA/JTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCAAGTCCCTCTGAGACTCCC ATGGATCATCTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616c	136 G A ---			CACACAAATTTGCAACACTTCAAAGTGAACGCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCCATACGTAGGTCTGGTCTCTCTATCACAATTGCCA C/GA/JTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCAAGTCCCTCTGAGACTCCC ATGGATCATCTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616b	141 C T ---			CACACAAATTTGCAACACTTCAAAGTGAACGCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCCATACGTAGGTCTGGTCTCTCTATCACAATTGCCA CGTAGC/C/JCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCAAGTCCCTCTGAGACTCCC ATGGATCATCTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-10616a	116 G C ---			CACACAAATTTGCAACACTTCAAAGTGAACGCCGACATCATCAGCCGTTAACGTCCAGGCCATGT CCACATAGAGAACGCTTTACTTCCACGTCTCTCCATACGTAGGTCTGGTCTCTCTATCACAATTG CCAGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTCAGGGCCCAAGTCCCTCTGAGACTCCC ATGGATCATCTCCTGTTCTGTATCAGGCAGTGATTTAACTCCTTTTTTGT
WI-1126c	52 G A ---			CTCTATTCTCTGGGCACTGCTTCTTTGGGGCAACTTCCAGTATCACT/GA/JATACTAATAATAA AAACCCGTGAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCCGCAAGAA AATTTTATTCTCAAGATATAAAAAATAAATAATTTAATTCAGTTTCTCAAAAGGAATATGAAT TGTTAAATGCAAAATCCAGCTGAACCTTTTTTGGACTTGCTTTATTCTTT
WI-1126b	230 T C ---			CTCTATTCTCTGGGCACTGCTTCTTTGGGGCAACTTCCAGTATCACTGATCACTAATAATAAAA CCCTGTAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCCGCAAGAAAT TTATTCTCAAGATATAAAAAATAAATAATTTAATTCAGTTTCTCAAAAGGAATATGAATTTGTT AAATGCAAAATCCAGCTGAACCTTTTTT/CJGGACTTGCTTTATTCTTT

WI-1126a	97	T C	---			CTCTATTCTCTGGGCACTGCTTTCTTTGGGGGCAAACTCCAGTATCACTGATCACTAATAATAAAAA CCCTGTAAGTCTGCTTTGCAATTTCAAGATTC/CAATATATATCCAGATTGTTTCCAGCAAGAAA ATTTTATTCTCAAGATATAAAAAATAAATAATTTAAATTCAGTTTCTCAAAAGGAATATGAAATTT GTTAAATGCAAAATCCAGCTGTAACCTTTTGGACTTGCTTTTATTTCTT
WI-11183c	124	C T	---			TAGTGCTAATTTTGGAAAAGTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTTAAATATTGGT ATGGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192	T C	---			TAGTGCTAATTTTGGAAAAGTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACATTT ATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTTAAATTC/CAATTGGT ATGGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118	C T	---			TAGTGCTAATTTTGGAAAAGTTGCTGATTTTAAAAATCTTTTAAACTTGAAAAATTTAGAGTAC ATATAATAAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCACATAACAA TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTTAAATATTGGT ATGGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174	G A	---			GCTTGGTTTGGCTTTAGTCTTATTGCTCAGTCTTGAGTCTCCCTTCTGCTGGCCCTTTTGATTTCA CCCATACCTCTATGCCCTGCTCAGACCAATTCCTCTATCTGGAGCGCTCTTCTTGACTTTCTCCTG TTCACCAACCTTCTTTTATTCTTCAGGACACTCA[G/A]TTCACATGCCACTCTCGTGACACTGCTCT TTCACATCTTCTGCTGCTGCTTTCC
WI-10770a	49	G T	---			GCTTGGTTTGGCTTTAGTCTTATTGCTCAGTCTTGAGTCTCCCTTCTG/TCCTGGCCCTTTTGATTT TCACCATACCTCTATGCCCTGCTCAGACCAATTCCTCTATCTGGAGCGCTCTTCTTGACTTTCTC CTGTTACCAACCTTCTTTTATTCTTCAGGACACTCAGTTCACATGCCACTCTCGTGACACTGCTCT TTCACATCTTCTGCTGCTGCTTTCC
WI-9667b	82	C T	---			GATGACAACTTCTGCTGTGACCCCTTAGTCTTGTCTCAGTCTGACACTTTCAATCTGCTGCTGATCATGG TTATCACTGGACA[C/T]AGCCACCTCCCGCAGCGCTTAGAACCTCATGAGTAAGGACCCCTGCTA ATGTCGCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCAATCT
WI-9667a	68	G C	---			GATGACAACTTCTGCTGTGACCCCTTAGTCTTGTCTCAGTCTGACACTTTCAATCTGCTGCTGATCATG G/C/TTATCACTGGACACAGCCACCTCCCGCAGCGCTTAGAACCTCATGAGTAAGGACCCCTGCTA ATGTCGCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTCTGTACCCAGTACCTAAGTCCAACTTGCAATCT

WI-10400d	189 A G ---			ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTAAGATGGTTAGCACACATGTAGCACTTACTAACACAATATTTATTCTAAATTT TCCTCCCTTACCTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCAGJTGCCATGTAG TTTTTGGTTCAATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10400c	166 A C ---			ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTAAGATGGTTAGCACACATGTAGCACTTACTAACACAATATTTATTCTAAATTT TCCTCCCTTACCTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCAATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10400b	165 A G ---			ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTAAGATGGTTAGCACACATGTAGCACTTACTAACACAATATTTATTCTAAATTT TCCTCCCTTACCTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCAATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10400a	46 T C ---			ACATTTTATTAGCAAAATCAGCAAAATATAAATAGAAAGTAATTCJTGCAATTCAGACATCT GCTGGTTAACTGTTAAGATGGTTAGCACACATGTAGCACTTACTAACACAATATTTATTCTA ATTTTCTTTCCCTTACCTTACTCTCCCAACCAAAATACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCAATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10809b	78 C T ---			AAAGGGCTACAACTAAGGCCAAACCAATGAACGGTATAAGGAGGGTAAATGCAAGGGGAGACCC CACCTCTCACCACJCTTTAGAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATACTGTTAG CAACAAATGGAATGTATTAGCCCAAGGCGAGGTATGGACCAAAAGTGCCAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---			AAAGGGCTACAACTAAGGCCAAACCAATGAACJCTTGGTATAAGGAGGGTAAATGCAAGGGGAGA CCCCACCTCTCACCCTTAGAAAGGGCATTTCAAGCACATTCATGAGGCTTCATATACTGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCGAGGTATGGACCAAAAGTGCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---			CGAGCTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATAGTGTAGATGCTGGGCTGTCTCTCCCTTCCAGGAATGCTGGGCCCCAGCTGGCCAGAC AAGAACTGTGAGGAAGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTGAT CATTTTATATGAATAAAGATCCTGCATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140 A C ---			CGAGCTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATAGTGTAGATGCTGGGCTGTCTCTCCCTTCCAGGAATGCTGGGCCCCAGCTGGCCAGAC AAGA/CJGACTGTCAGGAAGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAATAAAGATCCTGCATTTATGGTGTAGTTCTGA

WI-7038a	31	G A	---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGG[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAATACCTGAGATGCTGGGCTGCTCTCCCTCCAGGAATGCTGGCCCCCAGCCTGGCCA GACAAGAAGACTGTCAGGAAGGTCGGAGTCTGTAACCAAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAATAAAGATCCTGCTTTATGGTGTAGTTCTGA
WI-3429b	64	G T	---	---	ATACGCTTCTGTCTGTCCACAGTGAACCAAGCAGCACCAGGTGGCCAGGTCGGGCTCCACACA[G/T] CCCTCAGCCCCCTCAGCTTTCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATCCCAGTCTCCTCCTGGATTTGGATCTAGCAAGCAGAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-3429a	62	C T	---	---	ATACGCTTCTGTCTGTCCACAGTGAACCAAGCAGCACCAGGTGGCCAGGTCGGGCTCCACAC[CTAG CCCTCAGCCCCCTCAGCTTTCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATCCCAGTCTCCTCCTGGATTTGGATCTAGCAAGCAGAGACGGTCCCTAGAA TCCTGACTGTTAACAAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-6786c	151	G A	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATAAAGAGTGAGTGACGGTGACCT GTGAGCCCCATTCTTCT[G/A]TGGGATAAGGTGTCCATTGTTTCTTGGAGGGTGAATGCCACATT TTTTGGCAGGGGACACTCTTCTGGGTGCTCTATTGCTCAGTTTCATCAIT
WI-6786b	111	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGAT[TAAGAA]GTGAGTGACGGTGA CCTGTAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTGTTTCTTGGAGGGTGAATGCCACATT TTTTGGCAGGGGACACTCTTCTGGGTGCTCTATTGCTCAGTTTCATCAIT
WI-6786a	106	A T	---	---	ATTTAGGACAGTGAAAAAAGGGATTTATAATAAAATCTATGCCATCCAGGAGGTATGTGTCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAA[AT]GGATAAAGAGTGAGTGACGGTGA CCTGTAGCCCCATTCTTCTGTGGGATAAGGTGTCCATTGTTTCTTGGAGGGTGAATGCCACATT TTTTGGCAGGGGACACTCTTCTGGGTGCTCTATTGCTCAGTTTCATCAIT
WI-6711b	226	G T	---	---	GGCTATTTGTAATGCTTGGTATTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAACTTCACTTCCAATCACTGAAT TTCATATACCTCCATTATTAATCAATACATCATTTGCAGAGAAAAGACACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA[G/TTGGCA]ACTAAGTGTATCTCTAAA
WI-6711a	361	T C	---	---	GGCTATTTGTAATGCTTGGTATTGACTCCAAAATTGAATAAGTATTGGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCCCTAACTTCACTTCCAATCACTCT GAATTCATATACCTCCATTATTAATCAATACATCATTTGCAGAGAAAAGACACGGTGCCAACTG GGTTGGTTGGTGCCTGCACACCCACAGTGGCACTAAGTGTATCTCTAAA

WI-10613b	172	A C ---			ATTGATGCCAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTGAGCCATA TGGTGAATAATTTAGAAAGTATTATCTCTATATGTATATCTAGCTTTAACATCAATGAATGTGATTT TTTGCAACTTTTGACAAGGCCAGGCAATTTTATTTGAC/GCCCTAGGAGGTTACTATAATTTAGA AAGGCTCTTACCTTCCACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
WI-10613a	44	G A ---			ATTGATGCCAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTGAGCC ATATGGTGAATAATTTAGAAAGTATTATCTCTATATGTATATCTAGCTTTAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTTACCTTCCACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
WI-7587c	133	A T ---			GCTCTAGTGGGAAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCCCTTGAAGC ACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAAJA TJGGAATGAACCACTCCCTGCCATTCCTATAGAAATATCCCAAGACCCAGGCAATTTTGCCTCT TTCCACATGCCCTCATATGCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587b	81	G A ---			GCTCTAGTGGGAAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCCCTTGA AGCATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCTATAGAAATATCCCAAGACCCAGGCAATTTTGCCTCT TCCACATGCCCTCATATGCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-7587a	28	C T ---			GCTCTAGTGGGAAACCTCAGGTAGCTCCGGAAGATCTGTGCTTTCCAAAGTGACTACCCCTTGA AGCATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCTATAGAAATATCCCAAGACCCAGGCAATTTTGCCTCT TCCACATGCCCTCATATGCTGAGCCAACTGCACCTGGGGCTGCCCTC
WI-10681b	103	T A ---			ATGACTCAGGTGACAAAAGAGCATGCTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCAACC ACAGAAAAGCTAAGACATCCTTTTAAAGAGCCCTTAAAGACAGCCATTTTAAATCCTAATTCG TAGTTTATGATTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAGGAGTGACGCTCTGTTAAAG
WI-10681a	41	A T ---			ATGACTCAGGTGACAAAAGAGCATGCTCTAGACCCCATTTGACTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAGACATCCTTTTAAAGAGCCCTAAGAGAGCCATTTTAAATCCTAATTCG TAGTTTATGATTTCTCAAAATTTCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAGGAGTGACGCTCTGTTAAAG
WI-7222c	126	G T ---			GCCTCTCCTCACTGCTCGACCCAGGCTAGGAAAGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCTGTTCTCAAGTTGGGGATGGG/GTAAATA AGGAGGGGAATTCCTTGAACAAGAACTGGGGATAGTTATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGGTTGATTTTCAAGACTCGAATTCATTT

WI-7222b	255	G A	---			GCCTCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAGGGCTGCTTGAGATGACTGTGGTCCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTCTCAAGTTGGGGGATGGGGAATAAAGG AGGGGGAATTCCTTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGGTAAGGTTGATTTCAAAAGACTCGAAATTCATTTTCTCA
WI-7222a	126	G T	---			GCCTCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAGGGCTGCTTGAGATGACTGTGGTCCCCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCAACCCTGTCTCAAGTTGGGGGATGGG(GT)AATAA AGGAGGGGAATTCCTTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAAGTTGTATTTCAAAGACTCGAAATTCATTTT
WI-8054d	41	C A	---			AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTTC/AJTATCTCCTCCAGTTCAAAATG CTTGCACTTTTATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTGATACGCGCTTTCCCTGGGCGTACAGAGAAATCCTTGGCCCTT
WI-8054c	237	G T	---			AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTCTTATCTCCTCCAGTTCAAAATGCTT GCATCTTTTATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACA TCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCTTCC TGTCATAACGCGCTTTCCCTGGGCGTACAGA(GT)AATCCTTGGCCCTT
WI-8054b	148	T C	---			AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTCTTATCTCCTCCAGTTCAAAATGCTT GCATCTTTTATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAGCACA TCTCTTTGTAG(T/C)TTTAGCCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTGATACGCGCTTTCCCTGGGCGTACAGAGAAATCCTTGGCCCTT
WI-8054a	131	C G	---			AAAGATGACACTTAGAACTGGATCACTTGGCCCTTTCTCTTCTTATCTCCTCCAGTTCAAAATGCTT GCATCTTTTATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAACGCACCTCAAGCCTTAG(C/G)A CAATCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTTGGCCACCATAGCCACTCTGCT TCCTGTGATACGCGCTTTCCCTGGGCGTACAGAGAAATCCTTGGCCCTT
WI-10854b	152	G T	---			TTCCACAAAACCTTCCCTGGGCGGGTGACTAAGATGAGAAAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACACGAGACGATAGTTAACGTCTGGTAAGTTTAT ACGGTGTGCGAGGCAACA(GT)GGAGAGGTACGGGAATAGTTCTACTTCTCTTTTATTCTTGTG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102	C T	---			TTCCACAAAACCTTCCCTGGGCGGGTGACTAAGATGAGAAAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACA(C/G)GAGACGATAGTTAACGTCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGGAGGTACGGGAATAGTTCTACTTCTCTTTTATTCTTGTG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127	G A ---	---	---	AATTTATATGTGAAGGTTAGAAACTATGGCCACAGGCCCATTTCTAGCCATGCCTATTTTGTG TGCCTGATGGCTGTTGGTGTGACGAGTTGAGCCATTGTGACAGAGGCTGTTAT[G/A]GCCTT CAAAGCCAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTCTGCTGATTCTAGATAATTTAAA GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125	A T ---	---	---	AATTTATATGTGAAGGTTAGCAAACTATGGCCACAGGCCCATTTCTAGCCATGCCTATTTTGTG TGCCTGATGGCTGTTGGTGTGACGAGTTGAGCCATTGTGACAGAGGCTGTTAT[G/A]GGCCTTC AAAGCCAAAAAATTTACTCTCTGGCCTTGACGGGAAAGTTTCTGCTGATTCTAGATAATTTAAAG GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60	T G TGGGTTTT	TTGTTTGTGT	TGACATTATAT AAACGTAAAA GAAAATGT	CGGACACGTGTATATACAAATACAGATCGTATGGGTTTGTGTGGGTTTTTTTTTT[G/G]TTAC ATTTCTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A G AG	AAC TGCAAAAT AGGAAACCAG	CCACCTGGGGC TCCC	TTCAGTAACGTGCAAAATAGGAACACAGAG[G/G]GGAGCCCCAGGTGGGACAAATCATGGCTACCCCC TCCCAACAGAACAGGGGGAGGAGGTGGCCCCCTACACCCTTTAT
WI-8170b	259	G A ---	---	---	GGACTTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAGAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAAGGGCCCTCAAATGAAATCTACGGAACACATAACACAAGA
WI-8170a	204	T A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAGAACCCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGGAGAGATTTACAAGGTTAAGATCATGTGCCATCAAAAGTGCAATCCTATCAATCAGAA A/T/A/AAAGGTAAAGGGCCCTCAAATGAAATCTACGGAACACATAACAC
WI-8172	136	C G GACA	CCTTTATTAAA ATTGTTTCTT	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCTTAAGTCACTCTCCAATACTCCAGGTACATGGTGAAGAGTCACCTGTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACCTCCTTTATTTAAATTTGTTTCTTGACAT A/C/G/AGTACCTTTACAGGTATTACATTTCTCTCACCCGTTTACA
WI-8183	56	G A TGC	TGAAATAAAA ACAATTTCTGT	TGTGTTGAAAT CAACCTGC	AGCAGGGTTTGAATTTGATCCCTTATTTTACATGAAATAAAAACAATTTCTGTTGC[G/A]GCAGGTT TGATTTCAACACAGTTGATCTGTAAAAACCAAGCTCGTTTCTGATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83	C T ---	---	---	GCCTTTATTGGGATTGCAAGGTTACAAGGTTAAAGACAAAACCAAGCATGGGATTTTGC CGGAAAT ATTAGCGTTAAAGGAG[C/T]TGAGTTGAGTCAAAACACGGG
WI-8712	44	G A/G	CACAGGGAAG AGGTAGTGGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAAACAGCACAGGGAAGGTTAGTGGAG[G/A]GAGATGGTCAGGCTTCCTG TTCCCTAACAGCAGAGCCCCAGCAACCTAGAGCGCCTCACCTAGCCTCTTAAT

WI-8827	22 C T	TCCCCTGGGAG	GGGATTAGGAT	GGTGCCCTGGGAGACTATGG[C]/JAGTGAACACTAAAATCCTAATCGCCATGCATTGGAATTATT CCGACTATTACTTTCTTAGTTCCCTCTTATCCACCCAGCTCTTCT
WI-8833	51 A T	TCTTCATGCC	CCTCACACATT	CTCCGGCTCTTAAAGCTCTGTAGACTGCTCTCCATGCCATTCCTG[A]/JTGCCCTTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACCTGCCCTTGTCATAAAAGGTCAGCTATGT
WI-8377	63 A G	---	---	ATTTTTAGCCATGTGGTAAAGTTCAATTTTCAGTACATGGGTAACCCAGGCCCTTTCCC[A]/JT TATATCCAGGTATGCTACAAAGTTCTTTTAACTCTTATCAGAAGTTATTATTACTGTTCTTAGAGAG GCTACCAGGCTAAAAATTCACCTTAGTTGGTTGTCTAATGTCTCATTATTTATCCTGAAGCTCGTG
WI-8850	21 A G	GGGACTTAAC	CAACAGCCA	GAGGGACTTAACCTTTGGCCT[A]/JCCTGCCCTGGCTGTTGGCTCTGCGCTTGCTGTTTGGTTCTT TCTCTTCTACTGGCTCTTCTTTGCTTTGCCAGCCACCTATGCTGCTGT
WI-8853	79 C T	CCCGGCATTG	AGTCTTCCTGA	ACTTTCTTGAGCTGAGCAACCTCATCATCTTTAGCTTCTGGTTGATAACGCTGGTTAATCCCGGG CATTGAGGATA[C]/JATGGAAGGCTCAGGAAGACTTCATTCTCAA
WI-8865b	52 A G	---	---	AGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCAATGGTGAACA[A]/GJACAACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTCCATATAAA
WI-8865a	42 T C	CACAGACTGA	GGTAAGTCCGA	AGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCA[C]/JGGTGAACAACAACATGCT TCGGACTTACCAAAGGAGAGTCGAGCTTCCATATAAA
WI-8895	32 A C	---	---	GTGCCACAACCTGGACACCAACCAACAGAA[A]/CJCTCCGCTCCTTTGAAATTTCCATTAAAGAGCA CAATGGGGTAATTATACAGGGATGCTCCAATCGCTCTTC
WI-8456	93 G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGGGACTGATATTTGTGAAATATAATAAACTCTTTCC AAGGCTCCCATGCTTGGATGTCACA[G]/CJTATGTCAAGTTAATAAAGATTTCTAAGTGTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTCAACGGCAGACCACAAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCGCTGCTGCTCAGTCAACCCAC
WI-8496b	157 A G	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGATGGTAATGTTGTATCAGTGCATATTTCTATGGAAA ATTATATCTCAAGTAAGTACCTAGCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGGTCA AAGACACAATGCTGCCAATGCA[A]/GJTATATATAGAAATATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAAGTGGGATAAAACAGTAGCAGTGAC
WI-8496	41 G A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGATGGTAATGTTGTATCAGTGCATATTTCTATGG AAAAATTCATATCTCAAGTAAGTACCTAGCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATATACGCAGCTGTTAGAAAAAGTC TGTGGCCAAAGTGGGATAAAACAGTAGCAGTGAC
WI-14153	28 A G	GTGCAGGAAG	AACGGCAGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGG[A]/JTCCTCTCTGCCCTTGTACCCACATCCACAGAGCA GCCCTAGTCCAGGTGCGAGCCACTGCCACCCACGGCACAGGGAACAGGCCCATGCTGTC

WI-12108	40 C T A T A	TGAAAAGGG TTAAACTCAA ATTTC	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTTCTGGAAAAGGGTTAAACTCAAATATC[G]TAAATACTTTTCATTATACCAGGT CAAGAAAATGCCACAGCCAGAAAATTTATTTAA
WI-5989	29 G A C A C A G G C A	CCACAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAAAACGTCACAAAGGTCACAGGCA[G/A]CGTACATACGGTTCGTATACCCCATATATTAC CCCTTCATGTCTTAAAGAAGACATTTCTCTTAGAGATTTTCATTTTAGTGATCTTTAAAAAAAAT CTTGTTAACTTGCCTCCATCTTTTCTTGGTGAGGACACC
WI-12201	61 C T C T G C A T G	CCCCTGATCA CCTGCAITG	CCGACCACATA CCTGGC	ATAGTCTTTTAGCCTTTTCTCTGGAGTGTATGTCCCAAGCCCACTGATCACCTGCATG[C/T]GCCA GGTATGGTGGGGGTGATGGACGTGGTTTGCAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31 A T T C T G A C T T	GGCAGCCAGC TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAAGGACGCCAGCTCTGACTT[A/T]CTCTCTGTTCTGTCATCTCTCCCCCACATACCA ACTTCTCACCATGATGATTATACCAATAATACAGTTCCTTATATAGGGGCTCTGGAAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57 A G C C T C	TGGCCTCGCTG CCTC	AGGGATCAAA GAGAAAAGGC	TTTTTCGTTTGTATATGATCCGAATGCTTGAGAAGAAACCCCTGGCTCGCTC[A/G]GCOCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAGATGAGGTCCCAAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92 A G T T	CATGCCCTTTA AGGATTAAGT TT	TCITTTCTCTT TGAGTAGTGG	AGCATGTAAGGAGCAGTTTATTGATTGGTATATTACAGGTTTCTAACCCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAGTTAA[A/G]CCACACTACCAAAAGAGAAAAAGATTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109 T C A A T T	GTTGAGTATT GTTCTGCTCAT CAAT	GGGAAGGCTG GTACATATTGG	TCTGATGTCATTTATTGGCAAAAAATTATTCTGATACAACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTGTTCTGCTCATAATT[C]CCCAATATGTACCAGACCTTCCC
WI-12326	25 G A C A	GACAGACTTC AAAAGCAATT CA	AGGTTTGAAAA TATGTATTAAAG TACTTTGT	CTGACAGACTTCAAAAAGCAATTAC[G/A]CTTCAGAAATACAAAGTACTTAATACATATTTTCAAAC CTGTTTGCATTTCAAACAAAGTTAGCGTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63 C T ...		---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGGATATAGGAATTTTCAGCATATGTATTAT[C/T] TGAACATAATTTACAAAAGTGAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87 C T A T C A C A C C A	CAGACACAGC ATCACACCA	GACCTCCCGT GGC	ATACTGGTTTAATCCATGTCAAATGTAGTTTACAAAGGAAAGGACAAGTACCTTTTGTATAGAATAT ACAGACACAGCATCACACCA[C/T]AGGGCCCCACGGGAGGGTGGGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67 A G T T T T	GGGAGGAAAA TCCAATAAAT TTTT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTCTGGTGAATCTTTTAAGCAGGGAGGAAAAATCCAATAAATTTTTTAA[A/G]AAGGTTTAGCTATCCCAATGCTATTTAATACAATGAGGTTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11324	40 C G T G C C C C A	GGATAAAATCA TGTGCCCA	ATCAAGCTTTG GGGCTCT	AGCATCTGCATCTCCTTTATGGATAATCATGTCCCCA[C/G]AGAGCCCCAAAGCTTGATGACAT TCTGTAAGTTACAAAAATGTATCTGAAGAAGTTATCTGTCTTGICC

WI-11352a	69 T C G	AGCAGAC ATAGTGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTCCAGAAGGAGAGAGAGTCATCTACATAAGCACAGCACATAGTGGAA AGT[C]GCTAAGTGTCTACGAGAGGTCAGATCATATCCATAGAAAACAGCTCTCTTTTACTTGGCA CACCTTA
WI-11371	84 C T G	CAGCTGGAG ATTCTGATTCA	GOOCCGCGTGA GCAC	TTAGCCCATGCTGTCATTTCGAATCACCTGTGAACCTATGAAACCTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTGAGT[C]GTGCTCAGCGGGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGT GATTTCGATGCGTATAT
WI-11385	75 T C G	ACAGAAGACT TTCATATTCTT	GATTCTATTCT AGTCATGGTCA	CTTAAAGCATTATAGTTTGGCCTGATGGTGGACACAGAAGACTTTCATATTCTGTTTTTAAAGTC TCCTCAGT[C]AGGAAAAAGCTACAGATTTAAAAAATATGACCATGACTAGAAATAGATCAGC
WI-11388	88 C A	TGTTGAAATT ACACGTAAC	TGCCTTGTATC CAAGTTAAAAT	TCATGTGGCCAGTTAGCTCAGTTGGTTAGAGTGGAGCTCATAAAAAATTAAGAATGAATGTTTG AAATTACACGTAACCTAAGTTC[C]A/TATAATTTTAACTTGGATACAAAGGCATTGTTATGCTAAT
WI-11392	55 T G	GGTTATGTGT CTTGAACCTTA	GTACATTACAG TGTTTTGTAAA	TTCTATCATCCATTAAATGGCAGGTTATGTGTCTTGAACCTTAAATAATAC/T[G]CTTTTTTACA AAACACGTGAATGTACTTTCTTGTGAGAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACGTGT CATACTCCTCCCCAGA
WI-11396	52 A T	TTTTGTTTTG AAATGGTGT	AGCTTATTTTC ATATTCACCCA	AAAGAATAAGATGGCATTGTTTCAGTTAAATTTGTTTTGAAATGGTGTTTTAT/GATGGGTGAATA TGAAAAATAAGCTTACCTCATCCACTCTAAAGGGTAGTGGTGATTTTGAACCGTTGTCAAT
WI-11441	100 C A	TCCCCACCAAC CAGC	TGOCAGGGCCT TATTTG	CTGTCAGTCTTTCCCAACTAAACCGTGAGTCCAGTATGTCTGGCAGCACGCTGTCTGTCTTGGTG TATTCCTACTGAATCCCCACCACCAACGAG[C]A/JCAAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAAATGAAT
WI-11466	26 C T	TGAGAAGCCA TTTATTTTGCA	GTTTATTGTTA TAAAAATGAC	ACTTTGAGAAGCCATTATTTTGCAG[C]TCTTCAGTCCAAAAAAGTCAACATTTTCAGAATTTTT TATATAAGTTGTAGGTCAATTTTATAACAAATAAACTTCTATTATCTATTATCTCACATACATTT CATGTATCCTG
WI-13364	35 A G	---	---	TTTTCTTTTGTGCTCTTTTTTTAGTAGAAGC/A/GGGAACAGTTGTCAATACTACCTTCTGTTGG TCCCTCTTTAGACAACATACCTTCTTTTGAATGTAAAAATGTCA
WI-11276	41 A G	GGCAGOCAGG AGCAGAC	TGACTGAGGA GOOGGTG	AGGCAACACTGCTTTATTAGCCGGGCGAGCCAGGAGCAGAC/A/G/CACCGGCTCCTCAGTACACATT CCCCACCCCTGCTCGGTCTCCCTCCACTCAGGGCTGGGCAATGGAGGGGCGAGGTAGTCTGGAA
WI-12210	76 A G A	ACTGGGAAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTTCC	ATTGGAACAACCTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAAACA CTATTGCAT/A/G/GGAAAAACATATGCAAACTAGCATATTGTCTCTAGA
WI-14186b	88 A G	---	---	AATGGTCTGTTTTATTGAGAAGCTGTGGTCAATTTGATGGAAAGACACATACGGTACAAAAATTACA GGTGGTTAGTTCATTACATG/A/G/TACAAATCATTAGAGTCTTTACAAGTCAATTAGAGTCTTTGGAT TTT

WI-14186a	52 C T A	GGTCATTGAT GGAAAGACAC	AACTAAACCA CCTGTAATTTT GTACC	AATGGTCTGGTTTTATTGAGAAAGCTGTGGTCATTTGATGGAAGACACACATA/C/TJGGTACAAAATT ACAGGTGGTTAGTTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66 A G	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTTGGCTATAGGTCAGTGGTTCTAAAACTTGAGCTTGCAGAGAACACACTTGTGGGGCTTJ/V GTTCAACATGGACTGATAGTCCACCCCGAGATTTCTAAGTGGTGGTGGGTTG
WI-12345	37 C A	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAGAGGA/C/JCCTGAACCCCTCTGCAAGTATTCCT TTCCTGACCAGCTGGCTTGGCAGCTTTGTGAGATTGCAAAA
WI-13416	71 C A A A A	AAATTTTGG AAGTTTTTCAG	AGTGTATTATAG TTCAATGAATA ATTCAA	GAAAAGGCTGTAATTTTATTTTCAAAATTTTGGAAAGTTTTTCAAAAAAAATAAAATGACAAGAACA CATA/C/JA/AAATATTGAAATTTATTCATTGAACATATAAACACTTAGCAGAGGAAGGACTTTTGTAT
WI-12310	46 G A A A A G C	TTATCCCAAG TATAATTTTA	TGTTTAAATAT GTTGGGTCTT AAA	TTTGAAGAAGATGCTGAATTTATCCCAAGTATAATTTTAAAAAGCT/G/JTTTTAGGACCCCAACATA TTTAAACATCTTTACACATACAGAATTTTCAGTTTACAAATATCCAGAAAGGCAATTTTCTTAAGCAG T
WI-12086	72 C T	CCGGGAAAAC TTGGATT	GGAGTCTTCGG GTCITGG	GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACAAACACGTTTCCGGGAAAACCTTG GATTT/C/JCCAAGACCCGAGACTCTCCCAAGTCTCACTGTTAGTAAGGTCAATTTTGGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102 T G TTTTATG	GGCATAAAGT TCATAATATTC	GGAAAGTCTGT ACAAATCCC	ATGCTTTCACAGGTTGATTTTGTAAAGAGTTTGTCTATCTATAATTTTATTTATTTGGCATAAAGT TCATAATATCTTTTATGATCTTTTAAATATCTG/T/JGGGGATTGTACAGACTTTCCCTC
WI-11585	79 T C A A C A A A A	TGGGTTTGCAA TGATACTCC	CCATGCTTCAC TGATACTCC	TTAGAAGGAAGAAATAAAACACGGTAATGGGAAATCAGTTCAAGAGGTAGGAAGGAGCTGGGTT TGCAAAAACAAAAT/C/JGGAAGTATCAGTGAAGCATGGCCTAGAAAGTCCAGAGCAGGGGTAGAGT TT
WI-11604	68 G C ---		---	TTAGTTGGTTTCTGAAACITTTATGCTGTTTATTTTAAACATAGGATGTTCCAGTTACCAGCATTTI G/C/JAGAACTAGGGACTTTTCCATGAAATAATTAAGAGCTAAGGAATTTCTGACGCTCACCATTTTTC TTGTTACTCTGCAGTT
WI-11614c	108 C A ---		---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTTCAGTGTGAAACTGCA/C/AJATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11614a	60 A G CAGCTGCTTG	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAA ATGOC	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAAAATCCAGAAAGACTCAGCTGCTTG/J/GGG CATGTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAGTATTCGTCAGCTAC GGACTTCGT
WI-11626b	83 T C ---		---	TTGATTTTACTAAGGCTCTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAAAATAAA/C/JTACTTAATAAAGAAATTAGCCATACCACATTTGTTCCATTGCTAC AAGAACAATTTGGCAATGA

WI-11626a	39	G A G	TCACCTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGCTCTCCACTGGAACATGAAGGTAG[G/A]GATAAGTGTACAGGATAATATACT CAGATATTTTTAAAAATAAATTACTTAATAATAAGAAATTAGCCATACCACATTTGTTCCATTGGCTAC AAGAACAAATTGGCAATGA
WI-11627	23	T C	CCTTTCCTCC ATTGTCCTC	CATTTGCAACC CATCTCAAG	ACCCCTTTCCTCCATTGTCTCTG/C]CTTGAGATGGTGGTTCAAATGGGAAGTAAAGCAAAAAGGG AGATGAGAAATACTGATGCCCTTTTGTCTGGCTTACTTCCATTCCGATGTCAAGTCCATCCATG
WI-11636	61	A G	GGACTTAAAA AGATCTGCTTA TOCT	AGAAACTTGCT AAATATTTTAT GTAACACT	TCAGAAATGTTGCAAGCAAAATACTATTGTAAAGGTGGACTTAAAAAGATCTGCTTATCCT[A/G]TA TATCCACATAACTCTAGTGTTACATAAAAAATATTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTTGGTA
WI-11537	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAAATGAT T	GTACCATTTCTTATGGTGGCAATAAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAAATTTACAG TATACAATATTAGAGAAATATTATGTTGCAATTGCTCATCTTACTCTGACCAT[C/G]ATAATCATCTCT TTTGCTGGGTCCAGGACC
WI-11654	37	G C CTG	GCCAAAAGAC TATTCAGCAA	GGCTCTCCACG GACAGTTT	AGTAGAACATCAGTGCCTGCAAGACTATTGAGCAACTG[C/A]AACTGTCTCTGGAGAGCCACTCCAG AGCTATTCTAAGACTTTCTGTGGTTCATCATCTACTCAGAGTTCACACTCATATTTTCATATTTT ATTTTGGGTGTTGGGT
WI-11656	28	G A A A	ATTGATTTTAG AAGGAACTGC	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAACTGCAA[G/A]C]TTTACTTGAGGACAAAGCCTTGCCCTGCAGTTGTTT AAAATGTCTGAAACAATCAGATTCACAGCCTGGAT
WI-11680	55	T C ---		---	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCTTTT[C/]CTTGACATAAA GGCTGGGAAGGTGGTTTGGCCAGACCCGTACATCTTTT
WI-11696	47	T C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACTT	GTCCAAGAACAAAGATACTTTGACATCTTATCACAGCAGGGGACAG[C/A]AGGTTGGCTTCTCTA ATGCCACCATCTTGTTTTCAGAACTTTCCACTTCGCC
WI-11702	69	C T	GAATAATACT GAAATAACCA CAGCAG	AGAACAACCTT AAGCAAAATTAT ACTGAAA	TTACATGTGGTCAATGGTGACATACTTTCAATAATTAAAAATCGAATAATACTGAAATAACACACAGC AG[C/]TTTTCAGTATAATTGCTTAAGTTGTTCTAGAAAACACTGCTAATTTTTTGTCTCTGCAGA
WI-11706	60	C T	TGGCTGGAATT TTCTCTCTT	ATCACCAAAG AACAAATTCCA	TGCTGATTTCATCGCTTCTACCATCTGGCTGGAATTTTCTCTCTTGTAACAATTTATTGC[C/]GGCTG GAATTTGTTCTTTGGTGATTTGTCCCTTCCTGCT
WI-11709	105	T A	AGAAGCTTGC TTCAGTTGC	TCATTTCTCT AATTTTACGGG A	AATATCATCACTCATATCAGGGATGTTTATAAAAAATGAGAGATTATGTCCTTTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAAGCTTGCTTCAGTTTGC[T/A]GTCCCGTAAAAATTAGAGAAATGAAT GGCCAGATGGATGGAAAA
WI-11710	103	C A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCGAGCTTTCCAGCACACAACAGCCAGCCACACTCTAGACACGCCCTTCAG TCCAGTCCATCTGGCACCTAGCCCTCAGTCTTCACIC[A]CTCTCCCTCCCTCCACACACTCTTC

WI-11715b	123 C T	AGGCTGGCTGC AGCTT	TCCCCATCCTG TGGCT	AGAAATGGAGCTGTTGGGAGGACATGCACACAATGTAAACAGACAAAATGCATTACAACCTGGTGTGTAATGTGGCCACTATGAATCCCTATGTATAAGAGAAAGAGGCTGGCTGCAGCTT[C/T]AGCCAC AGGATGGGGACTGGGAAGA
WI-11715a	49 A C A A A	GCACACAATG TAAACAGAC A	CATTACACCAC AGTTGTAATGC A	AGAATGGAGCTGTTGGGAGGACATGCACACAATGTAAACAGACAAAATGCATTACAACCTGGTGTGTAATGTGGCCACTATGAATCCCTATGTATAAGAGAAAGAGGCTGGCTGCAGCTTACAAGCCAC AGGATGGGGACTGGGAAGA
WI-11727	43 G C T C A A C A	AACAATCCTT AAACAACATA	CCTGTGGTTG TGTTGCAG	CTGGATTTCTATACCTAACAATCCTTTAAACAACATATCAACA[G/C]CTGCAACACAAAACCCACAGGC AAAATGAAAACAGATGCCCCAGACAGACCCCAACCATGGCACACAC
WI-11728	16 C G ---	ATCTGTGGTTT TCGCCTG	---	TTTTATTATCAAACT[C/G]CAATTCATTTTCAAAAATGTAAGTTATCATCAGTCCCCATCCACTTT CTCCCATCTCTTATCTCTTTCCACCCCTACACTTTCTCTCCCTTACAACCCGGGTTCCAAA
WI-11758	61 A G T G C C T G	GCCTCAGAA GTATTTCTAA T	TGATGGCCCT GTGGTCTA	TTTTTCTCTTTTATTAAAGTCCGCTATATACTAAGAGGAGAACTGTGGTTTTOGCCCTG[A/G]TAG ACCACAGGGCCAATCACACAGCTTCTTGAGAGACATGGAGATGCCAAGATCACCATCA
WI-11295	37 A G A A T A T A A	GGCTCAGAA GTATTTCTAA T	AAAAGTGCTCA TCTGTGAATC T	COGGCCTCACAAGATATTTCTAAAATATAATTTGCTA[G/T]TAGAGTTACAGATGAGCAGCTTTTCA CAATTAGTGATGCAACAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93 T C ---	GGCTCAGAA GCAAGGGAA	---	AGCACATGATATTCGCTGGAGTTTCTGTGAGCTCAGCAACAGCAGAGTCAGAGATTAAAGAAAT ATTATTGCTCCTTTTTCCTCCCT[C/G]GTGATTGTTAATTAGGAGTCAAGGCCAAGTTATC
WI-11282	42 C G C C A A C C T C T G	GGCTCAGAA GCAAGGGAA	AAAACCTCAGA CTGTAAATTTT GTGTG	CATGACAACCTCTTTTATTAAATGGCTCAGAGAGCAAGGAA[C/G]CACACAAAATTTACAGTCTGA GTTTTGCGGCAGAGACCCCTCTCCACCTTTTTCATGCCTGTGTACACACACACTGTCCAAAGCCTC AGA
WI-11790	28 A G A A C C T C T G	CCCAACTTACC AAACCTCTG	CGGTAGGCGAG GCTAAGC	TAATCACCCAACTTACCAAACTCTGT[G/G]GCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61 C A A G T A T A C A	TCATCTAATCT GTGAGGTATTT AGTATACA	GATAGTTGAAC CTCTTCACTTT ATAAAA	TTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGATTATTAGTATACAG[C/A]AGT GATTTCTCTCTTTCTTTTATAAAGTGAAGAGGTTCAACTATCCAGACAGTCCCCTCTA
WI-12469b	91 C T A A G T T T A A A	GTTTTTAATGT GGTATTAGAA	CAATTTTCAGA TTGCTATAGC AAAC	TTTACTAAATTTCCATTTCTCCCTTTTATAGTTTTTAATGGTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATTTCTATTCTA[C/T]TGACAGCACAGTTCTTCAAAGTTTCTATAGACAAATCTGA AAATTGGGTTCTGAAC
WI-11906	52 A G A T C T G A A	TGTTATAACAT CAAGAAAGA	TTAATTTCTGC AGTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAAAGAAATCTGAAT[G/T]GAGGGAACTG CAGAAATTAACTTTCAGTCTAATTCAGAATGCCAGAGTAAGATGAACCTTTACAG

WI-11909	78 A G	TTTGTTGGG TGGTCAAG	CCTCTCTGAG ATTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCTAAATGGCTATTGTGTTG GGTGGTCAAG[A/G]CTATTTCAGAAAATCTCAGAGGAGGACAAATGATAGTGCACACTGCAGCCAGCTCG GACTGGCTTGAAGAGTC
WI-11806	60 T G	CATGAAGAGT GGGCAGTTCA	TOCTGTAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATTTGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[T/G]GTT TTATTAGTATATAAAATTGGCTTTACAGGAAGCATTATGG
WI-11946	31 C A	---	---	CCCTAGTGAATACAACCTTTGTCTCTGGAGAC[C/A]CCAGCTAGTCTAAGAAAACCTTCCTAGGCTGAG CTCTTTGGGAATCTAAGATAAAGAACTGAGATCCTGGGAAGAAGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTT GATT	CAGCTGTGGTG AATGTTGAT	ACAAAATTCACAAAGTACAACACTGCTTATTTCTTGCTTGAAGATCAGATCTCTGGTTTATTAA[T/ G]ATCAACATTCCACCACAGCTGAAGGAAATTAACCTGAACCT
WI-11027	90 T A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTGAAACTGCAGAAAGGGCAGGACAAAACAAATCACTTCATAGATTTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAT[A/A]AATAAAAAATCTGTAAACACATTTCTCATTTCTCTACGA ATACITTCITTTTGATATTGCAAAATTCATATGTCATACACAGAGGCACCTCCTCAATGCCCTG
WI-11049	95 C T	---	---	TTCTGCTGAAGATCACAAAACAAATTTCAACCTCTGTGGTTCAAAATAATTTAAGGATCTTGACCTTT GTGTTATTTCTGTTTCAACTAAGGAC[TAGACTT]CAGAGGCATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTCAATTTGTAGGAAGGAACATTTTCAAAAGCCCAA
WI-15488	69 C T	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAAAACATGGTAGGAAAAGTTCTCACTCTGCACTATAAAAAAGGACAGCCAGATATCA AC[C/T]GTTACAGAAATGAAATAAGATGGAAAATTTTAAACAAATTG
WI-13654	49 A G	AACAGTTAAT GAAACACATC OGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACACATCCGT[A/G]GTATGACATCATTT CACCAGCCAGCTACTTTCATGTGGCAGAAAAGGTAACCTTTTCCCATTTTACAGACAAAACCCAGT
WI-11070b	135 C T	---	---	ATGAGACCCTGCTTTGAACGTTAAACGTTTGGATAATGGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTTGGTGGTGCAGAGAGGTACTCCAAAGTA C[C/T]GTGGGGTCTGATGACTTCCAGGTCACCTGGGGATCCCAACAGAAAGGAA
WI-11070a	110 G T	CAGAAAATCA GCCAGCTATCT	TTGGAGTACCT CTCTGCACC	ATGAGACCCTGCTTTGAACGTTAAACGTTTGGATAATGGAAAAGGAGCTAGGACAATTTCTTGCTT TCAAGTAAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTTGGTGGCAGAGAGGTACTCCAA GTACCGTGGGGTCTGATGACTTCCACGGTCACTGGGGATCCCAACAGAAAGGAA
WI-12020	121 T C	---	---	AATCTTTTATTTCCAGCTGTTGAGACAGTATTTTGGGGCTGATTTACCTCTAGCGCGGAAACC AGAGCCAGCTATTAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCATT[T/C]CTCTTTTAGC ACGTTCTTTGTTCTCTC

WI-11076b	142	G A ---	---		CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCTGGCATCGGCTTATCTTCTGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGCAGGAGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGATTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-11076a	106	T C AGGCA	TCCTGCTCTGG GTATGTGAC		CATGGTTCTGCCAGCTTACAGGAAGCATGGTGGCTGGCATCGGCTTATCTTCTGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGCAGGAGAGAGAG GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGATTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-14263	49	T C GGCATATTCA	GGTATTCAAA AATTAGTATGG GACA		ACCTTTAAAGTTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAA[T/C]TGTCCTCCATACTAATT TTTGAATAACCTAACTACTCCCTTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA AATTATTGCTGAAATTAGGAAGGGAGCA[T/C]TGAAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAGCAAGTACCATTTTCCAAAGTATAAAACTCGTA
WI-14267	28	T C ---	---		GAITTTTAAAGTTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAA[T/C]TGTCCTCCATACTAATT TTTGAATAACCTAACTACTCCCTTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA AATTATTGCTGAAATTAGGAAGGGAGCA[T/C]TGAAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAGCAAGTACCATTTTCCAAAGTATAAAACTCGTA
WI-13892	50	G A TAGAAC	TGATGATGTCA TATACTAAAA ATCAAG		GAITTTTAAAGTTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAA[T/C]TGTCCTCCATACTAATT TTTGAATAACCTAACTACTCCCTTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA AATTATTGCTGAAATTAGGAAGGGAGCA[T/C]TGAAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAGCAAGTACCATTTTCCAAAGTATAAAACTCGTA
WI-15288	108	C G TCCCTCTCTC	AAAAGCTTCTT TCCCTTGA		ACCTCTTTCTGATGACACTTGTACCTGTAAAGGGTCTAGAGAAAGAGTAGTAGCTCTACTTTTGC TACAATTTCAGGATGACGGGCATGAGAGGATTCCTCTCTC[G/T]CCAAGGGAAGAAAGCTTTTGGC AATAATGGAAGAGGAGTGAACAAAGTAATGAACAAACAGCCAGATCAGAGGAAGAGATG GCTTTCTTTTAAATCTGGAGCA[G/C]JATTCAAGCAGCAATAATTTACTGAACACTTGCTATGTGCTG G
WI-13951b	88	G C ---	---		AATAATGGAAGAGGAGTGAACAAAGTAATGAACAAA[C/T]JAGACCCCGATCAGAGGAAGAG ATGGCTTTCTTGTAAATCTGGAGCAGATTCAAGCAGCAATAATTTACTGAACACTTGCTATGTGCTG G
WI-13951a	39	C T CAAAA	TTCTCTGATC TGGGGTCT		GAGACCAAAAAAGGCTCTTGCCCATG[A/T]ATTCCTGCTCTCCCTCTGATGACCCCAAGTGTCTT ACAATGAACATCCCTCAGCCCCCATGGCATGGTGCATCCCCCTCTCTTGGGATCTGTGAATATAACCA ACTGCTTGTCAATGGC
WI-13264	25	G A TTGCCAT	GGAGGGAGAG ACGGAATA		TTATTTGTCAATTAGCAAAAGGAAGTTAAATACTGATAG[A/C]GATGCAAAATTTGTCTTTTCATGCA TTTGTGGAGCAAGTACTAATCTGTCTGATGATTTCCCTCACAAGGAGTTGAGCCCTAGATGAC
WI-13960	39	A C TGATAGA	CATGAAAGGA CAAAATTTGCAT C		AATCTTTTATTTAGCTAGCCCCAGTGACTTTATGCATCTTATAACCAAGAGCCTTCAG[C/T]JAG AGCAAGCTGAGCCAGAGGTTTATCACACTTTGTCCTCAGGGTCCACCAGGAACAGGCTTGGCT
WI-15843	62	C T CAG	CTCTGGCTCAG ACTTGTCT		

WI-13983	52	G A	TCTCTCCACT CCTTAAACCT	CAATACTCTCT TAGCCACGTGG	TTGTGATCTGATTTCCGAAACATAGAAATCTCTCTCCACTCTCTAAACCT[G/A]CCACTGGGCTAA GAGAGTATTTGACAGAATATGCACTCACTGACTTAAACAGAAATTAGAACATCCAGGCACCTCACTGAGA
WI-13850	51	A G T T	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTGTAA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTAAACACAGCCAT[G/G]TTACAAACATTGT CAGGGAACATTTACAAGATAAATAAGATGGACTTGCAGGTGTAAAGATTACACTTCA
WI-15295	27	G C A	TGTCAGTTTGA ATGTATTCCTG	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCCTGAT[G/C]TTTCTTTGCCAACTATTCATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCAAGAAAAAGGCCCCGAAAAATATGAGTGAGACTCA
WI-14284	55	C T ---	CCGCTGCTATT CCCAGAT	GGTCTCTTCC ACCAAATCTT	ATTTCAAACAAATCCAGAACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAAACA[C/T]TATGCCAT GCGGGAATAAATGCTTATCCAGTGGAGCGCTCCCCTGATGCATTGA
WI-14288	85	G C	CCGCTGCTATT CCCAGAT	GGTCTCTTCC ACCAAATCTT	ATGACCAGACCAGAAAGCCCTGTTCTATATGAAAGACAAACAGGTGGCCATACCTTGGTGGAGGGATA CCGCTGCTATCCCAGAT[G/C]AAGATTGGTGAAGGAGACCATGACAGATGACAAACGG
WI-13522	33	C T	CCGCTGCTATT CCCAGAT	GGTCTCTTCC ACCAAATCTT	TTATTTTGTAGTTACCCCACTAATAACAAC[C/T]GAGAACCCTGACTTCAAATATTATGAGAG AAATTAATCCAGGGAAATTTTGCAGAGAAATAATA
WI-13529	42	T C	TTACCA	GCTT	AAATATGATTCCATTCACAAACATTTATTGAACAGTTACCAT[C/AAGCAAGAGAGTGAGAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCGAGGGGTTTAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84	G A ---	---	---	TTATTTGTCAGAAATTCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAAAGGAAACTAT[G/A]ACAAACAAGTATATATTTCAGGAAAGGACTCCTAGAACTTGAGCA ACA
WI-13536	29	T C ---	---	---	TGAAAGGATACAGAAAAAATCAGCGAAGT[C/G]GAAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCAGCTCCAGTTGTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52	G A ---	---	---	TTTATTGTTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCAC[G/A]AACTGTGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCCTTTGACGCCGGGCCCTTGAATCTGACATTTCAAGTCAC CGTAATAGAAACACAGAGCT
WI-13477b	61	A G ---	---	---	TTGGTTTTTAATACCTCTTGTGGATAAAAGGACATTTTTCATTAGCTTGTCTTCAAA[G/G]GAC AGAGAAATAAGATAAAATACCTTAAAGAAATTAATAGAAAAATTAAGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32	A G AAGG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA CAATG	TTGGTTTTTAATACCTCTTGTGGATAAAAGG[G/G]CATTGTTTTTCATTAGCTTGTCTTCAAAAGAC AGAGAAATAAGATAAAATACCTTAAAGAAATTAATAGAAAAATTAAGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACATTTATTTAGCATGCAATTTATTTCTGGCAATAAATTAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAG[AT]AAAAATGTTTCTGAATGTGCACACTAGATAATATATGCAGAATCCTTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAA	TCCATGTAATAATTTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAGAAATCAACA TGTGCACAAAAGAGATAAAATTT/GJACCAAAAAATTAAGATTTTTTGGGACAAATTCACATGTTT AAAAAT
WI-13582	43 C A	TGCAATCTAG AGACTGGGA	TCTGGGCAGTT AGATTCCA	AAGGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[CA]ATGGAAATCTAACTGGCAGAG AAATCAAGACCGATGGTGAAATCTGGGGCAGCTTCAAAATTTCTGCTCTTAAACATTTTCAC CCAATTTTTCATTATGGC
WI-13857	28 A G ---	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTTAGGTATCTGGCACAATTAACCAATGT CTGCCATTTTGTGTAGCTTTCATACAGTACAGATTTTCATTGATGTCGCTCCACATCTG
WI-15809	77 T G	TGGTTTCTGT TGTAATGOC	TAAGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTGCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAATGCTT/GJTTTACAAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T ---	---	---	TTAATCAGTCTGTGTCAGAAGAAACAGGACTTGATCAAGCTTCCAGCCCTCACCCTCTATCAGCA TAGCAATTTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAGAA[AT]GGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCTTTTATTCGAAGATGGGAAGCG[CA]CATTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACTCTA GCTGCAGTAACTAT/GJGATCCCATCCACTCTCTCTCTCTTTTGTGACTGAAACTCTTCAAGAACT GCTGAATGCTCTCTCTC
WI-15801a	24 G A	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAAATG	TCTTTTATTCGAAGATGGGAAGCG[CA]CATTTTCATTGGCTTGAATGAGAAAGCTTCATCTCCACT CTAGCTGCAGTAACTGATCCCATCCACTCTCTCTCTCTTTTGTGACTGAAACTCTTCAAGAACT GCTGAATGCTCTCTCTC
WI-13763	59 T C	GGCTGGACACT GCAGTGAT	CCACACCTGC CCCT	GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGGCTGGACACTGCAGTGATTT/CJAGGG GCAGGTGTGGGGCAGGGTGGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13578	48 T A AACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGTAAG AACATCTTTT GTC	TTTTTTTTGGTGAGTGTGCTTCAATAAAGAGCAGAAAGAAACCTT/AJAGACAAAAAGATGTT CTTACACACTGAGCTTACACAGTCAACCCCAACATGATATTTTGTCTTTTCCCGAGGGCAAAAAAGA GAGCTTCCAGAAACCTC
WI-13789	62 G A	TTGGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTG	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAAATGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTAGGCTCCTCACTCTCTT GAGGTCCCT
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAA	CCTTTGGGCA GTACTTTT	AATAACAAGTTTAAGTTGAGCTGCAATGTTGGCAATGCGAGTTTAAACACAGATCAAAAAAGC[G/AT]GCACAAAAAAGTACTGGCGCAAGGACAAAAAATATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15625	40 C T ---	---	---	GTTCCTCCACCTACTCCCGCAGAAAAAGGCATATTCAATC/TJTGTCCTCATACTAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCACACTGAA GACTCACAG	TOCCACCCCCA OCT	GTCTCATTCTGTCTAGGCTGTAAATTTTCAGTTTAAACAAGTTCTTATGTGATTTGTGGCCACACT GAAGACTCACAGAA/C/GJAGGGTGGGTGGGAATACTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCTCT
WI-13600	26 G T	TTAATGAGCC AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCACCTTAATGAGCCCAAGCATCCAT/GTJCCATCATCTAGTAACAATTTTCAATATGCACATTATAT TATACCTGGAACAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCAACCATCAGCAACCCCTCT TGATCCCTTCTCTACCC
WI-13602	89 G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAATATTTA ATATTAAT	GATAGGAAAGAAGAAATGAAGTCAATAGTCTTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCC CTTTCCATTCTGGAGACAACACA/G/JAAATCTATTATTAATTAATATTGTCATGAGGTATGCACCT GCGCA
WI-13650	76 A T	AAAGATTAC AATATTTCACT TTTAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTTT	GCATTAAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAAAAGATTCAATATTTTCAC TTTTAAACIATJTTAAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAGTTACCGG
WI-14319	83 C T A	CAATCAAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTGAATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG/C/JACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAATT
WI-13528	80 A G AAAA	CAATACATTT GCATTTTCCCTA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTAAAAATGGTAGCTTTTAAACTGTAAATCAATACATTTGCAATTTTCTTAAAA AAAGAAAGACATTTA/GJTTACAGAAAACTGTGGTATCATGCAGGAAAAAGCAGAAAAAAATTT
WI-13909c	93 A T ---	---	---	ACTTAAACTGGCTTATCTTACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCCCTCACACT CTCTTCAAACCTG/JA/AAATATCTTTTCAGAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	TTCTCACACT CTCTTCAAAC	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAAACTGGCTTATCTTACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCCCTCACACT CTCTTCAAACCTG/JA/AAATATCTTTTCAGAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A ---	---	---	TTTTTATTGAATTCCTCAATGTAGCAAAATCATTTAAACAAAATTAATAAAGGGACAGAAAAATTAAG AATCAACATCATCTCGGAC/JA/ATGGGAACCTTGAAAAAGGCATGGCAGTGGAGACCAAGTAACCTA
WI-14323a	78 T C ACATCA	ACAGAAAAAT TAAGAATCAA	GCCTTTTCAAG GTTCCCAT	TTTTTATTGAATTCCTCAATGTAGCAAAATCATTTAAACAAAATTAATAAAGGGACAGAAAAATTAAG AATCAACATCATCTCTGGACCATGGGAACCTTGAAAAAGGCATGGCAGTGGAGACCAAGTAACCTA
WI-15389b	104 G A AAA	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TOCCACACTT	AAAAATTGACAAATCAACTAGCTTGTCTTTTGTGCTTTTGGGAAGACTACCATTTATTCAAATTTATTATGT AATACACTCATCCAGATAATGAACAATCTGCGAAAA/G/JAAGTGTGGGAATCACCTCATCTGTGCG

WI-15389a	33 G A T C	AATCAACTAG CTTGCTTTTIG	TTTGAATAATG GTAGTCTTCCA AA	AAAAATTGACAAATCAACTAGCTTGCTTTTGTGTC[G/A]TTTGGGAAGACTACCATTTATTTCAAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAAGAGTGGGAATCAACCTCATCTGTGTC
WI-15747	88 T C A G T G T T	TGCTTCATTT AACTAATTT	CATAATTCACC AAAAGTTCATA TAATTT	TGTAATCTGCTTACAGTCCCTTGGCAAAGACAGACATATGTTTTGCATAAAGATATAAATTGCTTCAT TTTAAACTAATTAGTGTTTT[C/J]TTTAAATATATGAACCTTTTGGTGAATTTATGAAGTGTACCAAAAC C
WI-13752b	117 C T ---		---	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACCTGCGACGAGCTGAATGGCAGATGGT CTCTGCAGTAGTTCCTTCGTTAAGTGTGGATATACCTGGCTTGCAC[C/J]GGACACCTTTTACG GAGGGATTCGGACAAC
WI-13752a	106 T C A G T G T G G A	CCTTCTCGTTA AGTGTGGA	CCCTCCGTAAA AGGTGTCC	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACCTGCGACGAGCTGAATGGCAGATGGT CTCTGCAGTAGTTCCTTCGTTAAGTGTGGATATAC[C/J]GGCTTGCACCGGACACCTTTTACG GAGGGATTCGGACAAC
WI-14339	102 T G T T A C	CCCAATCAAA CAGTACATGA TTAC	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACACCTTCACTGGGTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACACCCCAATCAACACAGTACATGATTAGT[G/J]CGGTTTCCAGAAATCTGGATAC
WI-13744	115 C T A A A A C T G A A	TGGTGTGAAC GATAAGCACA GC	AATCAGGAAA GATAAGCACA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAACACGTAATGGAACCTCATGCAGCTTTAGAT TTCTTTGCCAGCTAGGAGCTTGTGTATGGTGTGAACAAAACGAA[C/J]GCTGTGCTTATCTTTC CTGATTCT
WI-14061	68 C T ---		---	CCTTGACTATATTGTTTTTCCAAAATAGGACTATGTGTAGAAGAGAGCCCCGTACATACCTTAT [C/J]AACCATTTTCATCCACCATTTGTAAAATCTCATCTTCTGGGTCTGGATACTCAAAAACAGAT
WI-15719	69 A C C A T T C A G C	ACCTTTTCATC CATTCAGC	TGATACTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAACTACACACTGAATATACTGAATTAACCTATTCAACCTTTTCATCCATTGAG C[A/C]AATTTAAAACCTTGCCCAAGTATCATGAACCTTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106 T C A A C T T	CTCTAAATCG ATACATCCAA AACTT	GAACTGATGCT TGCTGCTAAT T	TAATCCATCAATCTAAAATCACACATACTAGATCAAAACAGAAAGTACCACAGTATGCTTTATTTTGA GGTATTAAATGGTCTCTAAATCGATACATCCAAAACCTT[C/J]AGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27 G T C A C A	ATTTTATTCAC ATTAACCTTG	GTTCCTTGATA TGTCGCTTAGT TTT	GGATTTTATTCACATTAACCTTGCCACA[G/J]TAGCAAAAAAATCAAAACATAAACTAAGCCACA TATCAAGAACAATATACAATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA
WI-13785d	72 G A ---		---	TCAAACTGCACACTATAAAAGTGTCTTAAATGCAGCAGGAGATGTGAAGACACAAATGAAC AAGTGC[G/A]TAGTGACACATAGCTGTCAACACAGTG
WI-13785c	56 A C ---		---	TCAAACTGCACACTATAAAAGTGTCTTAAATGCAGCAGGAGATGTGAAGAC[A/C]CAAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACAGTG

WI-13785b	40	C	---	---	TGTTGTGACAG CTATGTGTAC T	TCAAACTGCACACTATAAAAGTGCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTCGCTAGTGACACATAGCTGTACACACACAGTG
WI-13785a	27	T	C	---	AAAAGTGCAC ACTATAAAAG TGCTT	TCAAACTGCACACTATAAAAGTGCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTCGCTAGTGACACATAGCTGTACACACACAGTG
WI-13793	88	C	G	---	GGATTTTACAT TCAGCCTAGAT ATAGG	AGAAACCAAGTATATCATAGGCAATAAATAAGTTTTTACCCCATTTGATACAACATAAGGGATTT TACATTCAGCCTAGATATAGG[C/G]AGTAACAATACTCTGCCATAAATCTATGACTTG
WI-13794	52	A	G	---	TTCTCACCCT TTCTTTCTC	TAGTCTCCTACAAATTCCTTCAATCCATTTTCTCCTCACCCCTTTCTTCTC[C/J]TACAAGGTTAAGA GCCCATTCCTCAACAAACAAAAACAACATAGAGCAAT
WI-15729	35	A	G	---	CTTTGAACCAT GTGTAGACTGC	TCATTTAAGTGCACTTTGAACCATGTGTAGACTGC[C/J]GGCACTTTAGAAAGAAGCTGAGACTGAA AAGTCTGTCTGACTTCCAAAGGAGGTAAAGTCCCTGTTTGAGCCCGGGGCTGCTCATTTGTTA
WI-13424	66	G	A	C	TGAGGTTTTTC ACCCTATCTT	GTCCCTTGACACAAGTCTCCCAACTGGTTTGAGGTTTCCCTTCTGAGGTTTTTACCCTTATCTTC[G/A] JTAGACCCCTGGGAGAGAAAAACACATGTGTAAAGTGGCTCAGGACATAGGCAGGCCGCTTCACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29	T	C	A	CTTTATAAAA GGTCAGAGGC AATT	AACTGTCTTATAAAAGGTGACAGGCAATTT[C/J]GAGATCCAGATTCAGCTTGCTCATATAAAAGAT TCAACTTCAAGTAGCACAATTCCTGCTGCTTTTAAATCCTGAACATTCCTGAAGCACGAA
WI-13446	22	G	C	T	GCCATGTTCTT TCACTCATCA	TGCCATGTTCTTTCACTCATCA[C/J]CCTTCTGATTTTGTATCCCTTCTGCTCTGTAATTTTCTTCTC TTCCCTTTTAGGGCCCTAGTCTGTTTAGAAATTCGGTTTTTGAGAGTAGTGAGCCCTTTTACTTTTT CTGACTGCCTAAT
WI-13725	56	A	C	T	TGAGCACATA TGGGTGOC	TCACACAAAGGCATTTTGGAAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[C/J]GCCCGAG ACAGCAGGATAAGTTTCAACAACTTGACCAGGCAGGTTAGAAAGCAAGGCATGGTTCAGGATG
WI-15702d	107	T	C	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAAATAAAGGCTTTCAAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCTGTAAACAA[C/J]ACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101	T	C	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAAATAAAGGCTTTCAAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/J]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90	C	T	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAAAATAAAGGCTTTCAAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAAC[C/J]CTGTAAACAATACTAATGGGTTCTTTGAACAAATAGTTT TGA

WI-15702a	48 G C	AACAAATAA AGGCTTTCAA AAAG	CCTCACCCCTT TACCCC	CAAATGTTTATGAAGAGACTCCGAACAAATAAAGGCTTCAAAG[G/C]GGGGTAAAGGGGTG AGGAAAGCATGTGAGAGAAACTGTAACCCCTGTAACAATACTAATGGTCTTTGAACAATAAGTTT TGA
WI-13831b	113 T C	---	---	TTTTTTTTTATGGATGCACCTGTTACATGTTTATTTAGCGAAGGTGACTTGGAAAAAGGAGATTACACAT ACTTCCACTGTATCCTCCGGGTAAGTTTCTCTCTCTGTAGAT[G/C]GTCTCCATGTTACAGTCAAC TATAAACATGGCTCA
WI-13831a	56 G C	---	---	TTTTTTTTTATGGATGCACCTGTTACATGTTTATTTAGCGAAGGTGACTTGGAAAA[G/C]GAGATTCA CATACTCCACTGTATCCTCCGGGTAAGTTTCTCTCTCTGTAGATGCTCCCATGTTACAGTCAAC TATAAACATGGCTCA
WI-13806	62 G A	---	---	TGATTGAGCTTAGAAAGGAAGTCATGTTGAAATCAGAGAGAGGCCAAAACCTAGGCCTCAGGT[G/A]C CCATTAAAGCATGCTGTGAATGCAAGGAAAGCTTAAAAAATTTTTTAAGGGTGACTCCAGTAAA CAT
WI-14372	86 A G	---	---	CACATTTTCAGCAACAAATCGAGGTGCAACACAGGGTTTATTTACATTAATATACTGGATTT TTTGCAATAAATAGGGA[G/G]TCTCTTTAAATAACCATCTCCCTCATTTGGOACGT
WI-14373	95 A G	---	---	AGGCTGTTTTTGAGGCCCTGAGGACCCCAACATGACACGTAAGCTGAACCATGGTCATGTGAGTT ATGAGCTAGGAACCCCTGGACGAAACCA[G/G]CACATATACAATCATCTCCACCTCCCAACGCCCTTT ACTTTCACAGCCTCTGCA
WI-14078	61 C T	AAAGAAGTAA ATTAGGAAGA GCAAGA	TGTGTGCATGT CTCTTACTGC	AGAAACCGAGAACTCAAAGAACCACATGGTGTATCAAAGAAGTAAATTAGGAAGAGCAAGA[C/T]G CAGTAAGAGACATGCACACAAATCGAAACAAGGGCATGGAGGAGACTTTAGATGGTCACG
WI-14083	47 C T	AGACTTGAGA GCTTAAACA ACACT	GOCTACTGGAC CTCTAAACTAC TGA	TTGCTACATAACACATTACTCCAGACTTGAGAGCTTAAACAACACTC/TATTTGTTATTTTACACAG CTCAGTAGTTAGAGGTCCAGTAGGCTTGGCTGAGTTGTTGCTTAAGGCTTTACAAGGCCAA
WI-14085	31 A G	CAITTAATTTTC ATGTGTAAGA AGAAAA	CAGTCATGTTT ACGTGCTAGTT	TGCATTTATTTTCATGTGTAAAGAAGAAAAAC[G/G]TAACCTAGCAGCTGAACATGACTGCATGGATAC ACGGCTCAGCACGAGGCTAAAGTCAGAAAGTGAAGTGAAGAAAAAATAGCATGTTGATTTAAGTGAAA TAACAGAACAGGAGGCCCTT
WI-12169	121 G C	AATAAAACTT CCTATTTCCTT TTGCTT	GGGTTCTGAGG TGAAAGAAAA A	GTCAAAGGTGGCAAATTTTATTTCCACTTATCAAGAACTTACAAAAATTTTTGTTTCATTTCTAAA TTTTCAACCTTATGCTAAGTTATAAAATAAAACTCTCTATTTCTTTTGCTT[G/C]TTTTTTCTTTCA CCTCAGAACCCCTTA
WI-15705	50 A G	GGAGGGAGAT TTTAGACTGA ATC	AGCTGTAGTCG TCAAATACTCT AGAA	TTGTTTTTATTTGGGAGAATGAAGGAGGAGGAGATTTTAGACTGAATC[G/G]TTCTAGAGTATTT GACGACTACAGCTCCTCTCTCTTTGTACTACGAGAGACCCTGCTTATAGCCCCCAACAGGAAATCCTCA TCTGGGTTGGCAGACAG

WI-14379	102	C T	TCTATTAAACA GGGTTATGTCA CACC	ATCATCTGTT TGAGGTTGACA	TTTATGCTGTTGTTTCTACTGGTGGTCTCGCTCACTAATATCAATCCTAGTATGATTTCTTT TACTTGCTGCTATTAAAGGGTTATGTCACACC[C/T]GTCAACCTCAAAACAGATGATACT TAAATAAAACAAAGCAGAAA[C/A]CCACCAATTAAAGAGGACACTGCAGAGGCTTATGTACA ACACGTGTCCTCCGCGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22	C A	ACCGCAGAGCTGCTGATTTAAAA[A/G]ACAAGCGTCTGGATCTCTCAGGGGCTGGACCAGCTGC AGTGGGGCTCCGGCACTGCTCTGCTCTCCAGGACTCTTCCACCACCCC
WI-15937	24	A G A	CGCAGAGCTG CTGTATTTAAA G A	GCAGAGATCCA GACGCTGT	TGAACTGAAACGTATTTCTCCA[A/C]ACACCGTAGAACTTAAAGGCCGCAAAAGACTCACACCC ACCACCTAGCGCGCAAAAGGAAGTTTCAGGTGATACAAGATGCTCCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24	A C A	AAACTGAAAC GTATTTCTCC A	GGCCTTTAAGT TTCTACGGTG	ATGTTTTATGATCAATTTCCAAACATACAGTACAGGGAAGGTGAATGAGTAAGAAAAAATCAT ATTTAAGTCCCGTTAACACTAAGCC[A/G]TATTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14124	92	A G	GACAAAGGCGAGTTTCTGTAGTTCCAGCAGGGCCAGAGCAGTTATCAGAACGGGTTGACCT GCATAGATTTTTCAGGACTA[C/T]GTGGCCATGCCATTCTCTGAAGTGAAATTAATGAACA
WI-14125	88	C T	CATAGATTTT G C C A C	GGATTGACCTG GGAATGGCATG G C C A C	GTTTATTTCTCAGAGTTCTGGAGGTTAGAGTCTGAGATGAGGATATCACCAGCATGGTTAGGTTCT GGTGAAGACTCTCTGGCTTACAGCTGGCTGCTTTCTCACCATGTCTTCACAT[G/A]GCCCAAAGAGAC AGAACAAGCTCTCTGGT
WI-14136	120	G A	ATGCTTTCACA A	CTTTGGGC CAGTATGTACA GTGACATAACA	TTGTTTGGCACCAGAAAAGCT[C/T]ATGTTCTATGTTATGTCACTGTACATACTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTTGTTTCAATG
WI-14138	23	C T	GAAAAGCT A	TAGAACA GCTCATTTCTT	GGCAGGTTTATTCATAATTTTCAAAACTTGAAGCAACCAAGATGTCCTTCAGTAGTAGTATTTCA GACAATC[G/A]AATATTACTTAGCACTAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-13551	74	G A	GACAATC A	TAATATT	TTTTTAAAGAGTGCTCTCACATCAT[T/G]TATATTGATTGCACACAAAACTTTTTAACTC[C/T]GTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGATAGAAGCCTTCTTCAGAATCA CCTCC
WI-15953b	59	C T	TTTTTAAAGAGTGCTCTCACATCAT[T/G]TATATTGATTGCACACAAAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGATAGAAGCCTTCTTCAGAATCA CCTCC
WI-15953a	26	T G A T	TTTTAAGAGTG TCCTTCACATC A	TCATCTGTTCT TGTTGTTTTG A	TTTTTAAAGAGTGCTCTCACATCAT[T/G]TATATTGATTGCACACAAAACTTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGATAGAAGCCTTCTTCAGAATCA CCTCC

WI-14631	82	G A	---	---	TGAATTCATGGACAGTTTTGCCTCTGTTTGTAGTGAAACCCCTCACAGCACTCTGCATAGTCCGCTTT CTGCTCTTTTAAAC[G/A]TGCCTGGTCCCTCTGCCAAACTTTTAGGATTGGCCCTCCTCAGGGCCTT GTCCTGA
WI-6053	24	A G	---	---	ATCACACCGGTGCTAAGAACAAC[A/G]TCTTCATGTCCAACATATCCCCGGGACTTTGTCAACTG CAGTACACTTCTGCAATTGAACCTGGCTTCTCTGGAGGAAGCCTCTAGAGCCAGGTAAGGGGTGC AGCAGTGAGGGGTATATCTGGGCTGGCCAGTTGGAACACCGAG
WI-15964	99	T A	CTGGAGTA	GACTTCTCCAC CCTCTTGC	CAGAAACCTCTTCTGTGATTAAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGCGAGGCTGCCTT GGGAGGTAGTAAGCTCTCTGCTCCCTGGAGGTAT[A/G]CAAGAGGGTGGAGAGTCTTGGCAAG
WI-12075	103	G A	GGCAC	CCCCTTCTTTC TCCTCCCTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAAGCAAAAGCCAGGCAATACCCCATCAG AGACAGTGACAAGAGCAGCTGGGGGCACGGGGAGGC[G/A]GAAGGAAGAGAAAGAGGGGAGGAG CCT
WI-12179	96	G A	TGGAGTCA	TCGAATGACCC TGATAGTC	TAATTTAAAAACACGCCCTTCCACATAGTGCCTGAGGCATCTGCACATTTCTAGAGGACATGA ATAGTGATGTGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCAATTCAGGAGGAACAG
WI-14651	49	C G	ATTGT	GGAGATATTGA TCCTTTTCTGA CTTATT	CACAAATAGTGAAATTATCTGAGCAAGATCATCTCTCATTTAAATTTG[C/G]AAATAAGTCAGAA AAGATCAATATCTCCCTGCTTCAAAATGACACTCCCAATTTTACAGGTAACCACTGTTA
WI-14666	105	T A	---	---	AATGTGGACTTTCAACAAGGGTTAAACATACTAATAACAACCTTCTACAACACATTCAGAGCAT TATAACAAGAAATTATTCAGAGCAGCTAATGTATTAAT[A/A]AACCATGAAAGAAAAAATTTG ATCTAGATGTCAGCAAAATGGCTGAGACTG[C/T]TGCTGTGTAGATGCAGTGTGTGTATGTTCTAC TCTATTACAAAAATTAACAGAAATATGGCTTCGCTTTGTGCAATGTTTATATCACAGTC
WI-13967	103	A C	AAATAAAA	TTGTGTTTCA TCTCTAAAAG TG	AATTTAATAGCAGCTCTGTGTGTGATTTTAAAGAACAAAGATAAAATATGTCATTCAGCAGTCATTT AAAAATAAAGACTACAGATACAAGGAAATAAAA[A/C]CACTTTTAGGAGATGAAAACACAAA
WI-14408	60	T A	G	TTAATTGTGTA AAACTCATTTG TTACTTT	TTAATATTCAGCAAGTTATTGCAACAGGTGAAAAATGCAGACACACTATTACAGGCTG[T/A]AAA GTAACAAATGAGTTTTACACAATTAATAATTAAACATACCTTATGGGATTTGTGAATGA
WI-13683	47	C G	---	---	TTTTGTGTTAAGAACAGCAATTTGAAAAATAAACCTATCTGCCCATG[C/G]TTTACAGCCTTTTAAAT TTGTAATATTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63	C T	CGTCT	CATTGAGATAA AGCACACTTAT CAC	TTAGAAAACCTGATAAAGCAACACAACTTTTGGGGAAGCACCATGGCAGCTCCTTTGTGCTA[C/T] GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
WI-14635	22	G A	---	---	ACATGGCAGATACAGAGCTGTC[G/A]TCTTGAAGAACACCACTGACCAGGAAATGCCACTTTTACAA AATCATCCCCCTTTTCATGATTGGAACAGTTTCTGACCCGCTCTGGAGCGTTGAAGGTGACCAGC ACATTTGCACATGCAAAA

WI-16002	59 T C	GATAACATAA AATGATCATG AGAAATTC	GCCATCTCTC TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAATTTCA/T/CJGTTA AAAGTCAAAGAGGAGATGGCTAATGCATGCTGGCT
WI-15361b	101 A G A	CCCACTTGAAC TCAAGTCATC	AAACTAAAG CTTTGTGCCTA AAA	GTGGAATTTTATTAAAGCATCAAAATTTCTTTCACACTCAATACTGTTGAACAACAGATAACACAT CTTCTTGCTCATCCACTTGAAGTCAAGTCATCA/GJTTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTAAACCA
WI-14759	73 T C	GGGTTTGACTT GTGGGG	TCCACACTGC OOC	TGAGTTACAACAAATGAGCAACAAGTTAGAAAAATTTGGTTTTATTCAAACCTTCCCTAGCGTTTGACTT GTGGGGT/CJGTACTCAATGGGGGCGAGTGTGGGACGGGAGGATTGCAACCCAGAGTTTCATACTG CAA
WI-12535	50 A T T A T	CTAGGAGGGTT GAGGTGTAGA	GCTCCACGAGA AGAGAGGAA	TCCTAACATTTATTCAGGTGGTGAAGGGTTGAGGTGTAGATA/TJCTTCTCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCGTTCTGTGTTTATCAGCTGAGAAGGCGAGTCTCGCCATC TTAAAGACCTGCGCTCC
WI-13805a	112 G A GGGAA	AAAGGCACAC	CTCAGCCTGOC TTGACC	TTCCATTTCATTATGCTTGGCTTTACCAATTTTTATAGCTATTGGGAGGCAAGGAAATTTTGGC CCAGAAACCATGAGATTTGGGTCAGAAAAAGGCACACGGGAA/GA/JGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18 T C ---		---	ACACAATATAATTCCTAT/T/CJCGAGTGATTAAAAACCTATTTGTTGTTTAGAACCAACAAAACTAC AAGAAAAACATTTTCAAAACCTTTTTTTTTCAGGCTGA
WI-14808	52 T A CTACCTGT	ACCCACACA	GAGGCATCACA ATGTTAAGATT TT	CTTTGAACACCTTTAAGCAACAGTTAAAAAGTACCCACACACTACCCTGT/T/AJAAAACTTTAAC ATTGTGATGCCTCTGCATCAATTTTAGAAAAACAAAGAAACACAACTGAAGGCCCCCATGTA
WI-14816	29 A T ---		---	AGTTAAAAAAATCGAGTCAGCATTTATT/TJAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCTGAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAAGCTACGACTTC
WI-12542c	71 G T ---		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTATCCATGTGAGGGCTCTAGATC ATG/GT/TAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70 G T ---		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTATCCATGTGAGGGCTCTAGATC AT/GT/TAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45 C T TTTAAA	GCTATTAGGC AAACTGAACA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57 C T CAAAAA	GGATACAGCA GTAAAGAATA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATTTCTAGAAACTGGGGATACAGCAGTAAAGAAATACAAAAATCCTGC/C/TCTTATA GAGCATACATTTAGAGGTGGGAAAGAGGCAATAAATA

WI-14836	28 T C ---		---	TCITTTGGAGGGATAGAGGACAGAGTGTTC[C]GTTGATTTTCGTTTCGGTTTCAGTTTGGTTGTCATT GGTTTTTGTITTTTGTCTAATTTTGGCCCAACCCTATAAAAAGCAGTGCACCCAGAGGCAG
WI-14856	60 A T A A	TGGTGACAG GAAATACTT	TTTGTGCTA CTTTTACAAA CTTT	ACATTTCTTATGATAGCAACAATAATATGATGGATGGTGACACGGAAAAATACITTAAT[AT]TAA AGTTTGTAAAAAGTAGCAACAACAAAATTGAGTATATATACTATAAGTGATAGAGGATGTATATGAAAAA GGCTATAAAAAGCTCCAAAA
WI-14863	61 G A ---		---	ATGGCAATTTACTTTATAGCAATGAACAAATATTTGTCAAAGGGCAAAATATTTTGTCTG[G/A]AG TTAATAAGTTAATATCTTTACCACAAAGCTAGAGGTCAACAGTACCACATATTATTGATTGCCACT ACCTGGC
WI-14867	46 T C A	GACATCCAA GGCTCTCTAAC	TGGGGCTGCAG ACACTC	TTTTAATTAAACGTAAAAAGGCAGGACATTCCAAGGCTCTCTAACA[T/C]GAGTGTCTGCAGCCCCCA TTGGCTTTGAGATGTGAATGTGTTAACCCAGGGTGGA
WI-14733	98 G A A	CCAAATTGAC AGATATTCTGC	GATGAGGTGAG GCCATTATT	ACGGAGTGGTCTCTGATGTATTCTTGTCAAAAAATGTTTGCCTGATTCTAATCATGAAAGAACAAATT AGAAAAATCCAAATTGACAGATATTCTGCA[G/A]AATAAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAAA
WI-14898b	79 A C ---		---	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCATACATAGGTGCCACTAAGGAAA ACTTCTCCATAC/AAGCTGCCTGCTGTGCACGTTGCCTGGGCTTTGCTAACCCCTGGTGTGCATCT GGCTGTGTTCTGCTT
WI-14898a	50 A C C A	CATGTACAGG AAGAGTTGTCT	AAGTTTCCCTT AGTGGCACCT	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCATACATAGGTGCCACTAAGG AAAACTTTCTCCATAAAGCTGCCTGCTGTGCACGTTGCTGGGCTTTGCTAACCCCTGGTGTGCATC TGCTGTGTTCTGCTT
WI-14907	48 G A G G A C T C T G A C	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGTATTATTTCGGACATTACTGTAGAGGCACACATTGGACTCTGAC[G/A]ATTCCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGGCACACCCCAATCAATCAGTGACTCCTGCACTGCAGAGGGGCCACATG CACGATGCTCACGTGTG
WI-14911	52 G A C	CCAATACATT CAGTTCTGTT	CAAAACCAGGA AAAGGACCTT	CTAGAATCTGGGAAGTCCAAGCTCAGTGCAACCAATACATTCAAGTTCTCTGGT[C/G/A]AAGGTCTTTTC CTGGTTGCAGACAGATACCTTGTGTATCTCCTCAGATGGCAGAGAAAGAGAGAAATATCT
WI-14913	88 C A ---		---	CTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCAAGCAATTC TAGTGATAGTAGAGGACTCA[C/A]CCTGCACGTGCACCTTTTCATATACAGATCAACCAATCCAAAC CTACACCTCCAACCCCT
WI-14914	66 G C A	CTGGACACAG TTTTCTCTAGC	CAAGCCAGGA CAATAAATTC	ATTTCCTTGATTGGCTGTGTAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTCTCTAGCA[G/] C[GAA]TTATTGCTCGGGCTTGATGGCTTTCACAGC
WI-14926	49 T C ---		---	GTTTATTTTCAAAATGACACATCCAGATTGAAATGGGCACCTTAGCGAA[T/C]ACTTGTGGACCACA AGACTTGTCTGAGAACATGTTCAAAGACAGTTTCAAATAAAAAATTTCCCTTAATCAGGTCCA

WI-16083	89	C T	A A A A A A A A A A C A A C A T A T C A A G G A T	T G G A A A A G A T T O A G O O C	G C A T C T T T A T T A C C A G A A A C T A T T A T G T C C T T A A T C A T T G T T T A A T A T A T A T A A G C A T G T T T A A C A C A A A C A T A T C A A G G A T C T G G G C T G G A A T C T T T T C C A T T C T A T A G A A A A G C A C T A A C C A T C C A T T A A A G C A G
WI-14930	55	C T	G G A G G A G T C C C T C A T G G A T	C A C A A C C A A C C A A T A C C G C	C A G T T C T G T T C T G A A C A G C T C T C T T T C C A C A G G A G A G T C C C T C A T G G A T C T G C G G T A T T G G T T G G T G T G G T G A T T G G G A G C A C G A G G A G A G C A A
WI-14946	47	T C	---	---	T C A A T A C T G A A G G T G T C A A A G T G G T C T A T T T G C C C C C A G A C A T A A C A T C T C T A A A T C A T C C T C T A G A T C A G G A G T C A T A A G G A C C A T T A A G G C T C A T T A C A C A C A G T A C T T T A T G A A A G G A T T
WI-15987b	80	A G	---	---	A C A T T A A A C A G C A C A A T T A A G G G T C C C A A C G A G G T T G G T A G T G C C T T C C A C T A T G T G A G G A C A C T A A G A A G A T G G T C A G T A T A G A A C C A A G C T G C G G T G C C A T G C T C T T A A A C C T C T C A G C
WI-15987a	32	C T	C A C A A T T A A A G G G T C C C A A	G G A A G G C A C T A C C A A C C T C	A C A T T A A A C A G C A C A A T T A A G G G T C C C A A C T A A G G T T G G T A G T G C C T T C C A C T A T G T G A G G A C A C T A A G A A G A T G G T C A T C T A T A A C C A A G C T G C C G T G C C A T G C T C T T A A A C C T C T C A G C
WI-14948	56	T C G	A G G G A A A C T G C T A A C T T G T C A G	G A T G A T C T T A C A T C A G T T G T T G G A	G A A T A A A A G T C T T A T T G C C G T T C C T C A G G G A A C A G G A A A C T G C T A A C T T G T C A G T C T C C A A C A A C T G A T G T A A G A T C A T C T C T G A C C A T A G O G A A C C T G T A A G G C T T G C T C C C T C C A G C T G A
WI-16100	52	A G T T G A	C A A A A A G C T A T T T C C T A C A C	A C A G G A A T G C A G A A A A C A G T A T A T T A C	T T G T T A A A T T C A T C A A G G A A T T G A C A A A A A G C T A T T T T C C T A C A C T T G A C A G T C A G T A A T A T A C T G T T T T C T G A C A T T C C T G T T A T C A A C T C C T C T G A A A A T C
WI-14958	83	A G C A A G G G	A A T A A T T T A T C T C T T T C T T T	A A T G C A T T C A T T T G G G T T T T	G T G A T T A T C T G T A A T T A T T G G G A T T A T T A T T C A A C T A A A A T C C A A G A T G A A A A T A A T T A T C T C T T C T T T T C A A G G A G A G A A A A C C C A A A T A A T G C A T T T T C A G T T T C C A G G C C T T T G A A C T G C A G C A G A A A A T T C A A G G A
WI-14976	35	C T T C G T T C A A A G	G T T G A T T T G C T T C G T T C A A A G	T C A A A C T A A A T C T T C C A T T C T A A G C	T A T T T T T T A A T T G G T T G A T T T G C T T C G T T C A A A G C T G C T T A G A A T G G A A G A T T T A G T T G A G G A G G G G C A G G T T T G G G G T A G G C T C A G C G G G C A T A G T G G C C A C A A G A A G A T G C C C A T C T C A C A C C T G G A G A C G T C C A T G A G C A C C T C G
WI-14981	31	G T T	T C A G T G G T G T T T A T T G G A T T T	C A C C T C T G A C A T A A T A C T A G C A T A A A	T A A T T G A T T C A G T G G T T T A T T G G A T T T T G T T T A T G C T A A G T A A T T A T T G T C A G A G G T G G A G A A T A A A G A G G A A A A A A A C A A A G T G G G C T C G C A T C A A C G A C C T G A T C T T G T C A C A G G A A G T T T T T G A G A G C T C A C A A A
WI-14992	80	C T G A A G C T G C A G	T G C A T T A A A T G A A G C T G C A G	G C T A T G T G C T C A G C T T T C C T	T G A T T A C A T T T T T A A A A T C A T G C C T A C C A G C C C A T C T A A G C C A A A T T C A A A C A C C A C T C T G C A T T A A A T G A A G C T G C A G C T A G G A A A G C T G A G C A C A T A G C A C C C A A C T A G T A T G G A A A G A A A A C G T A
WI-15002	72	T A	---	---	A A A T C T C T C T T C C A C A C A C A G A T G A A C T T T A A T A A A T T A C A A A T G C A C C T G A A A A T G C C T T C T T G A T T T C C T A T T C A G T T A G G C C T C A A A T G G G C T C T C C T C A A G G C T G G A C C T C A A A G G C C C A G T T
WI-15000	90	G A G T C T A A	G A C A G A A A A A G A C T C A G A C T	G T T T C T A G T T C T G C A C A A A C T T C A	T C A A G C C A A A T A T C T G C A C A A A T A A C A T G T A T T G A A A G G T A T A G A A A T A A A C A G A T G G A T A G A C A G A A A A A G A C T C A G A C T G T C T A A G T A G A T G A A G T T G T G C A G A A C T A G A A A C A A A A A T C C A C C T

WI-12323	68	G A	CACA TACTT CATGTACCTAT	CACTGGACATA TTCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTATACACAATACCTTCTATGTACCTATGAAATAA G/AJACAGGTAGGAATATGTCCAGTGCACACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91	A T A A C A	AAGGGACGAT TTAGTATCTAA	GGCATGTCCCA GTGTTTTT	CATAAGTTGCATTATTCACGTCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAACA/A/TJCAAAAAAACACTGGGACATGCCCCCTGAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100	C A T	CCTGCCCTTAT ATTGGAATTC	GGGAGAACCATG GGTCTCT	ATTTGTTGTTTATTTAGCACCTGAATTTAGGCAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCCCTTATATTGGAATTTCTA/C/AJAGAGACCCATGGTCTCCCCAAGTGAGGAAGCC AGGCACTCAGCCCTTC
WI-14712	38	T A C A	TGAATGCTTCC AAGTACAAAT	TGAAAGTATGT TGTATATGGTA	TTTGGTGCTACTTTGTGAATGCTTCCAAAGTACAAATCA/T/AJCTCACAATACCATATACAAACATACT TTCAATCACAACTCAAATATAAATAACCTACAAAATCACATTGC
WI-13712	40	A C T C T A T T G	TTTACTTTGTT GTCAATTTTAT	CCATAAGGTCT CACACTTTTCT	TGGGATACCCCTTTACTTTGTTGTCATTTTATTTCTATTG/AJCTTATAAGAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGGCAATATGCAATAATAATTGTGTGTTTAAATTTATGCAAT
WI-16163	35	C T A	TCTGGTGATGC AATTGAAATA	GC TGCCAATTA CATTAACTTAC	TCTAAGATTTTACTCTGGTGATGCAATTGAAATAA/C/TJATTGTAAGTTAATGTAATTGGCAGCATT GCCCAAGGTTAAGAGGACTATTCTTTAAACAAAGACAGTGCTGACATTTATTTCAGGT
WI-13453	88	T A T C	AATGCACAAA ATCTTGCTCT	TCAGATTTTAA CATCTCTTCT	TTTTTTTATTGCAATTTGAGTGCTTTATATATTGGGAAATTGCAGTGATATAACATTTGTACAAAT GCACAAAATCTGTCTCTCT/TJATGCTAGAAAAGAGATGTAAAAATCTGACCTAGTTGAACAGTCTT AATGAACTCATTGICCAT
WI-16167	58	T C G A T T T T	CGCACTCTAA ATTAGAGATA	TGCTGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTCTGATATACATT/T/CJCATCTT ATTCCACGAGCAGCACACCACACGACAGTAGAACAGTTCACACCTGATAAAATGCAACAAGATG
WI-14482	17	G A ---	---	---	GCAGAACCAATTAAATAA/G/AJAATCTGCAAGTTTCCCAAGAACTCTGGAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGAAATAAAGGACTGCTGTATGTGACAGTCACTGGT
WI-15069	81	T C ---	---	---	TGTAGTCTTCAAAAGACATGTGGCAGATAGCCAGGCCATCTATGTGTATTCOCAGTATCATGTAC GCACTAAAAAAAT/CJGTGTGCTGCTGCTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C C C A G A G T G C	TGAAGATTAA CCAGAGTGGC	AATTGTGTGCA TTTTGAAGAGA	ATCTGATTTGTGTATCCCAAGATATACAGATACTCTATAAACCAACCCCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTGGC/CJCTCTCTTCAAAATGCACACAATTAAGACG
WI-15012	59	G T A T G T	GCAGCAAGAT TACATCAGTA	CTCCAAATAGC CTAGAGTATAG	CATGGCAGCAAGATTACATCAGTAATGTAATAATAATACAGCTTTTTTTCATTGAAGCTTTTGT/TACCTT TACTATACTCTAGGCTATTGGAGTGTCCCCAC

WI-15100	74	G A ---			---	TCATTACAGCCAGAAAAATACCCAAATATTTCCAAATAAGCAAAAAATTTGGAACAGACTGGA GTGAGAAC[G]A/GGTTCCACCACCAAGCCCCCTCAAGACAAGATGGACACGGCAGCTGGTTCTGGGGT GCATTTCTAGTGGACTTTAT
WI-14492	92	A T AATTACT			TAAGAC	TGGTACAGAATGTTTAATTACAGCAGGCGAGTGATTCCAGTTAAATAAAATTTAAACCTTTATTTT CCCAAATATAAAAATTACTAAATTTAA[A/T]GTCCTTAAAGAAAATATAACATGGTGACAGCTTT
WI-12002c	89	T C ---			---	TCTTTAATTTTATCGGAATCCAGGACACAAAGAAAAACACCCAAAAACCCACATGGAGACAGAAG ACGAGACACAACCTCTCCCCCACT[G]GCCCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGGTGAGAC AG
WI-12002b	68	G A ---			---	TCTTTAATTTTATCGGAATCCAGGACACAAAGAAAAACACCCAAAAACCCACATGGAGACAGAAG AC[G/A]AGACACAACCTCTCCCCCACTGCCCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGGTGAGAC AG
WI-12002a	30	C G GGACACAA		TCGGAATCCA	TGGTTTTGGG TGTTTTCTT	TCTTTAATTTTATCGGAATCCAGGACACAA[G/C]AAGAAAAACACCCAAAAACCCACATGGAGACAG AAGACGAGACACAACCTCTCCCCCACTGCCCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGGTGAGAC AG
WI-15116	96	C T GTTGCAGTAA		GGGAGCCCTA	CCTGAATATGC AATTATTTAT ATGACA	TTTTCATTTATTTTCCAGAAAAAGAAATCACATTTTCAGTAACAACCTTACATATAGAAATTAACCTTTG TTCTGGAAATGGGAGCCCTAGTTGCAGTAA[C/T]GTGTCATAATAATAAATTCATATTCAGGATTTTG TGAATAGGTGATTGGGA
WI-12578	37	C T AATGGGAA		GGCCTAAAGG	TCAAGCGACCA CCAACAC	GCAAAAGCAAAGCTATGGAGGCCCTAAAGGAATGGGA[C/T]GTGTTGGTGGTGGCTTGATACCTTGGT GCTGTGTGCATGGAGCAGAAAGTCTTCCCTGGTCCATGCAGGGGGCTCACATATTTTAACTGCACATAAT TTGGGCAAACTGTCATT
WI-15153	40	A G GCATTGCA		CCCTTATGTTG	AACCTCAGATA AGTGCAGTGTCT	ATTTACAGTTGGCCAAAGATCTCCCTTATGTTGGCATTGCA[G/A]GAGACACTGCACCTTATCTGAGGTTA GAAAAAATGTAGTCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATACCATTTCCCTAA
WI-15215	84	G C TCAAATGGG		TGGCTTTAGAA	CCAACAGGGGA AAAGTCA	CCTTTGCTCTCTGAACCTGGGACCAGGATGTGAATAATTTTGAATCTGATGCAGGTGAGGTATGGC TTTAGAATCAAATGGG[G/C]TGACTTTTTCCCTGTTGGTGGAAAACTCTGTGAGGGTTTGGCA
WI-15225	80	C T C		CTTGAGGACCT	TTTGATTGGCA TAATCACTCC	AGGAAAGAGTGGTAAAGCAAAGCCGATCATTTGGATGGAATGATTATGTGTACAGCAGCACTTGAGGAC CTAGAAAGCAAAC[C/T]GGAGTGATTATGCCAATCAAATTCGAAGTTGGAGATATGCTAAAA
WI-15152	51	G A ---			---	AATTTGCTAGTGCAAAATGGACCAAGATTTGGAAGGGCTATGTAACACACA[G/A]TATGCACACCAC AGCCATGTCAAGTGTACAGATGCTCTGTGTGCTTACGCTTCTTAAAAACACATCAAAAGGCTGCA
WI-15123	55	C T TAGGATG		TGTTAGTGACA GACAGATAAA	TTGCTTAAGGG CAACAGAC	TGACTGTATACCAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACTCACTGGGGAAGAAACAGACATGCAACACAGAGATAAAACACAAT

WI-15182	49	C A	GCACAACCAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACACTAGCTAGCTGCACAACACAGGGGCAAAATAC/AJTGCTGGATTAAACCC ATGCTAATGGGTTACCTTTATTAGTAATCATGGGTCCCTCATAAGCATGGTCCAGATCCG
WI-15198	38	T C	GGGOCCTGGC ACTATG	ACTATCCGTC AGGCAGAGTAG	GTGGACCTCTACAAGTACCATGGGCCCTTGGCACTATGTC/CTACTCTGCCTGACGGATAAGTTGGC ATATGGTTTCAGATTGCTTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12601	42	T C	CATTTATTGAG TATTCCTGCTT	GTGTAGTCTT ACATGCTTACG	TCAAGTGGTAAATAGCCATTTATTGAGTATCTTGCTTTGATT/CJGCTACGTAAGCATGTAAGACT ACAACATTACGACCCCATCTCTTCAAGAGAGGAAGTCTGGTATTATGGAAAAACATTTTGTCTATTCAGAT T
WI-14510	104	A T	TGGCAAAATA TGCATAACAA	TTGAAAATGGT TAAACTGGCA	ATGTTGAGAGTAATAATATGCCCTACATATTTAGTGTAAGTACACCCACAGATATTTTGGGGAAGAG TTGTTTGTCTTTTGTGGCAAAATATGCATAACAAAAT/AJTGCCAGTTTAAACCATTTTCAAGAGT
WI-15239	57	T C	CATTTGCAAT AAACACCATC	GGACCTTATCT GTGGACTCAGG	CAGTGTATGACATTTCAATGGGAAAAAGATTGTGCAATTTGCAATAAACACCATCATTC/CJCTGAG TCCACAGATAAGTCCCGGAGAAAGGGCTTCCCTCTCTCTCGCTGGTGGTGGTTCACGTTCCCACTCCCGAGT GAAGCCTTTCTGGAATG
WI-12634	52	T C	GCATCATATG AACTGTCTAGC	GGACAAATTTGT AAACATAGCT	ATGAGTTTATAAACTGGAGACAGCGCATCATATGAACCTGTCTAGCAGTATTAT/CJGCTATTAGCTA TGTTTACAATTTGTCTGAAGGGTCTAGATGTGTACACCCACAGAAAGTGGTGAATTCCTGA
WI-15249	34	T C	GGGCTTGACAC AAAGTTCTAA	GGAAAGCCAG AGATTTTAAAC	TTTGTCTGAAGGGCTTGACACAAAGTTCTAACTTT/CJTTGTTAAATCTCTGGCTTCTCTGGCTGG TGAGGAGGCACAGGCTGGGCTCTTCAAGTATCCACTGTGTCCCGCATCTGTCCCTCCCACTCCCGAG CCACATTTCTGGCTCT
WI-12159	28	T C	AAGACACCGT GCAAATGC	CCCTCTCTCTA GTGCATTT	CTGTCCGGGGAAGACACACCGTGCAAAATGC/CJAAAGTGCCTGAGGAGAGGGAGGGTCTGTGACTC CCAAACCTCGAATATTTTATGAATCTAAGAGTCCAGACGCGAGTTTCATCCACGGAGATCTGC
WI-12648	41	A G	CCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC	TCCCAGATTGTATGGAATGCCTAGTGGCATTAAAGGATGC/A/GJTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACACTACTCCATGTTAGGTGCTTTACTTGGATTATCTCAGTTAAAAACCAACA
WI-12684	64	T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTCAGTAAACCATGCTGTAACACAGCTGTGC/G/ TJCCATTAGGCTTTGTGTTCCATTTAGAGAGCACAGGAGAGGAAATTTAGCATAATCTT
WI-15260	75	A G	AAAGGATGAA GCTAATCATG	TCTCTCCAGG AGCTTGC	TTTATAAGCTGAATGAAGAGGTGACACAGCGGACACTGTCTAAGTGGAAACAAAGGATGAAGCT AATCATGGA/G/AJGCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGAAAAATTAA TCTGT
WI-15325	39	T C	CATGTGGCTGG GAGGC	CCCTCCACCAT GATTGTGA	AAGGTTTAATGGACTCACAGTTCCATGTGGCTGGGAGGTC/CJTCACAATCATGTTGGGAAGGCAAAA GGCACATCTTACATGGTGGAGTCAAGAGAGAATGAGAGC
WI-13936	123	C T	AGTTGGCATTC AATAGCCTAT	TGAAAACCTCCA CATGGAGTT	TATTTGAGTATTTTCATCCATGGGCTTCTCACTCCCTATACATTCCTCAGGGTTGAGGTAGTCTACCC CCATAGGTTTCAGAACCTATGACCTGTATCTTTCAGTTGGCATTCATAGCCTATC/CJAACTCCATGT GGGAGTTTCATAATAA

WI-14528	62	T G	TTTAACTTTT TCTGGATGGTA TAAAT	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTAAATATATTTTAACTTTTCTGGATGGTATAAATTT/GJTT GAATTATAAATTTTAAATTTTATAAAGTGCTAATCGAGACATCACTGGGTATAATTGA TATTTCTTCGGTTTCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAGGAAAAAGA ACAAATTT/CJCAAVAGACTTGGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA CG
WI-15347	74	C T	GACTTCAAAG GAAAAGAACA AATTT	TCACTCCCCCA AGTCTTTG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTAGAGAGACTACTTCTCCTGGGACCAGC CAATTTCTAGTAGTAGAGGACTCA/CJ/CCTGCACGTGCACCTTTTCATATACAGATCA TTTATGGCTGTCTCTGTAATACAATGTGGTGAANAAC/GA/JCTTAATTCAGGACATCTTCCACCTTG TTTTGGCTCCAGTTGACTGCAAGACCAGTGCAGGCACATAGGCTGATTAATCAGTGG
WI-14546	95	C A	CCAATTTCTAG TGATAGTAGA GGACTCA	AAGGTGCACGT GCAGG	AGAAATTTTCTTTTTTAACAGGACAAGTAAACAGATTACATCAAACTTCAGAACTTCTCAAATAC CTAGTTATTATACACATTTCCCATCTGTCTTGCAG/JGAGGGGATCTTGGTCGGCTTAACA CCAGCTGGAGGTGGAATAAATGCGGCAACCACAGAAAAACACACAGCTACACACAGGCCTGCATT TGGCTTAT/CJGTGCTGAAAAAGAGGGCCGACCTCTTGATAAAGAAATGCT
WI-15353	37	G A	---	---	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAAATGCACACGACATCACGAGTAAATACTG TTTGGTAAACCTTGTTTCAGTTAAATATGTAT/CJGTGCCGTGCATGTCATGATTAATATCTCTCT TACCACAGTCAACCCTAAAGAACCAAGCTTAGGACTAGGGACACAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTTAATGCCGACGCCGACACCCACA
WI-8039b	97	T C	---	---	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAAATGCACACGACATCACGAGTAAATACTG TTTGGTAAACCTTGTTTCAGTT/CJAAATATGTATGTGCCGTGCATGTCATGATTAATATCTCTCT TACCACAGTCAACCCTAAAGAACCAAGCTTAGGACTAGGGACACAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTTAATGCCGACGCCGACACCCACA
WI-8039a	87	T C	---	---	AAGTAGAACACAATAGAAATGGCTCAAAAATATCAGAAATGCACACGACATCACGAGTAAATACTG TTTGGTAAACCTTGTTTCAGTT/CJAAATATGTATGTGCCGTGCATGTCATGATTAATATCTCTCT TACCACAGTCAACCCTAAAGAACCAAGCTTAGGACTAGGGACACAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTGAGATGATGATTTTAATGCCGACGCCGACACCCACA
WI-8044	107	C A	---	---	CACAACATTCAGAAAGTTTTCTGCAATGTGTCTCTCTGATGTCTTAAAAAGATTTGAGCTTTGACTAT ACGATTTCCACACTGAACGCATTCATAAGGTTCTCC/CJ/AJGATGAGGATTTCTGATGATTAATA AGCCCGAATCTGGCTAAAGGCTTTCCACATTCAGACATTTGTAAGGTTTTCTCCAGTGTGGAC TCTCTGGTGTGCACAAGATGGAACCTTCGGCTGAATGCTTTCCACACT
WI-8550	32	G A	GGGAACATCA ATGCAACAAG	TTTGTGGCTTG AGTTTACAAT T	CTTACTACATGGGAACATCAATGCAACAAGTA/G/AJAATTTGTAACTCAAGCCACAACTTAGTTA ATAATCATGGTTAAGGGACATTCGCAAGAGCAACTGATGCCTCAGTGAA
WI-8057	87	T A	---	---	TATTAGATAAAACCTTTGTTCCCGATTCCAGGATGTTAAATTTGCTTCTTTAAACTCTGTGACTTTT CCTGGTTCAAAGGACAGTT/AJGATGGACAGCAGCAGGAGTGGGGTCTGAAAAATGTAATCTTT GTGTAAGGCACACTCTGTGGCTCACAACACTGCCCTGTGAGAGGGATGCTGCCTCCAGCCCTAAAG ACACTAGGGCTTTCAATGGACGGGGTGTGAAGCAGCCAGATGGTAAGG

[illegible]

WI-6375	28 A	GGTTATTGCA TATGGAAATC GAA	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAATCAATAG[A/G]TATCTTTTACAAAAAAGGTTAGATAAAGATCTC ACATTTGTAAAGGCACATATGAACATTTTATAGCAAGCACAAAGGCGAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA[T/A]GCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T	A ---	---	TTGTGCTCAACAGATGAAATTCATAACCTTGTTTCTGATAAGACAAATTCAAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A	T ---	---	CTAATATAATCCTGGGCACATGGATCCAAGAGAGATTTTGACGACAGATTTCATTATAGTTACTTAA CAGCTAAATAATAAGGGTGATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G/T]ATCAACCTTCCCTAAGCATCTGTCTGTGTCGG CAGC
WI-6523	165 G	T CCTG	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGAAACAGGAAGATGGGC TCTGGAGTCCAAACAGGATGTGGACGTCCCTGGTAGTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCAGTCAGGTGGACCTTCACAACAACAGCAAGCTAAACCTCTGAGAGAAAAAC[C/G]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C	G ---	---	ATTGTAATTAATAATTTACATGGGCTATTTTAAAGGACATTTGTGTAATGTTTCCACTTTGTTTTAAA [C/T]AATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAAGTTTGAAAAATGGGCG
WI-6558b	68 C	T ---	---	ATTGTAATTAATAATTTACATGGGCTATTTTAAAGGACATTT[G/C]TGTAATGTTTCCACTTTGTTTT AAACAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAAGTTTGAAAAATGGGCG
WI-6558a	42 G	C ---	---	AACCAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAAA AGTTGTCATA[T/C]AGCAATGGATGCTGTGTCAGAACATCTGCCAATAAATTAAGAAAAAAGGA ACTCAATGAAGTTACTGTTATATAAACAGGAGCTCACAGCAGGATGTAAAGATTATGGAAGAT ATCGTGAGGCCAAAAAC
WI-6629	75 T	C GTCATA	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATCAAAACTCCAGCTGTTTCTGCTCTTT TTACTTAGCAAGGAAACTTTAGTGAATGCTACTTGACAAGAGAAAGTCACTTTCTCAAGCACAC[A T/C]ACCAAACTTGAAGGTGATTGAACCCAAAATAATGGTGGGAAACACCAAAATGAGGTGGAGGA ATGAGAAAGATGTGTGGCCAAAGCTATCTGGTTATATTTTGATGTTGCCAAT
WI-6644	134 T	C ---	---	TGCTAAACACCACCATTTAAGGAGAGTACTAGGAAAAAACTACCAACACAGCATGTGAAACAGT TGGGCACGGTGGTAAAGGGCACAGACTCTGGAGCCACAG[C/T]GGCTAATACACTGCAATATTTTA TGTTAGCAATATAGCTGGTCTGTGTATTAACCAAGAGAGGGTATCTGG
WI-6690b	106 C	T AGCCACAGC	ACATAAAATA TTGCAGTGAT TAGCC	

WI-6690a	28 T	C	AAACACCACG ATTATTAAGG AGAG	GCTGTGTTGG TAGTTTTCT	TGCTAAACACCACCATTAATTAAAGGAGTTCJACTAGGAAAACTACCAACACACGCGCATGTGAAAC AGTTGGGCACGGTGGTAAAGGACACAGACTCTGGAGCCACAGCCGGCTATACACTGCAATATTTTA TGTTAGCAATTATAGCTGGTCTGTGTATACCAAGAGAGCGGTATCTGG
WI-6770	53 A	G	CAACCCCAA AACATCACA	GTATAATAGTA TGAATAA	GATGTTTAATGACACAGATCTCCCAAAGTAATCCAAACCCCAAAACATCACAAGJAATTATTTCAT ACTATTATACACTCCAAAGCAAAATACCTCAACTGCAATCC
WI-6686	151 A	G A	GCAITCTTCCA AAACAAAGA	CCTGTAAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTTGAGCAAAATCAGTACGCACTAATCTTGACCAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTAAATTTAGATGAAATTCACATTTAAACATGGTAACCTCCAAGCATTTCT TCCAAACAAAGAATAGJAACATTTGGAATAGTCACTTACAAGGAC
WI-6761	32 C	A G	GATCTAACAG CTGCAGAAATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGCGAGATCTAACAGCTGCAGAAATGGCJAJCTTCTTCCCTCCAGCTTTTGTGAACAAAC AATCTCTAAGGCATCAGAAAGCACTGAGTGCAGAAATGGGTGTTTCAGGTACAAAGTCTC
WI-6844	225 T	C ---		---	TAAATACTGCCAACTAGCATTACGTCCACTCTTGCACTATTGCACTATTAAACAAAGGGTATTTCCCTTG GTATTTCAAATGATGCATTATACAATAAACGAAAGTTAGAACTTAAATGCACCTGATTAATTATG TAACTGGTAATTTGTTTTAAAGCAATAAATTTGGTCTCTTCTCATAAATGGAATTTTAA TATTTCTGATAGTCTTGAGGTTCJATCATATTAGTAGTGCAAGTGTG
WI-6824	112 A	G ---		---	CGGTTTTGTACACTTTAATGGTTTTTTTTAAGGATTTTTTTCAGGTCTTGTGCAACATCAA ACAAAGGTACTGAGTACTCCACAGGGTACAGAGTCTGCCAAAGJACACCTTAGAAAAATTACAT GACCGGAGAAATGGCTCTTGTCTCTGAAGAGCTTACAGTCTAGGATTTGACAACTCACAGT CTTAGGAAGTGGGCAAGTAAGGCAATTTCTCATCCCTAGAGCTATTGTG
WI-6889	139 T	C AATC	GAAAAATGAG ATGCAGTTAA	TCACITTTGGG CTTTTAATTAT TCT	GTACAAAAAGCTGAGAAAGGACCAACATGGAAGTGTCAAGAAACATTTCTGATAGGTACGGACAA AAGAGCTCCTTCAATCAAAAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTCJAJAGAATAATTAAAGCCACAAAGTGAAACTGTTGTTCTGGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T	C ---		---	TCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACCTCAAAATATCTGATGAACCTTGATGAACGAA AAGAGGTCTCCTTAAACAAGATATCATCTCCGAAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAGAAAACTTTGCCTCCCAAGGAATGTGTTCTAATTTGGTTTCAAGCAGACTGGTTCC CACTTTTACCACITTCJCATGACATTGGACAATAGTACTACTCTTTCTAC
WI-9413	112 G	C ---		---	GCCAGTCTCTAGTAAGTCTCTAGGGACATGACCAGACCAGAGCCCTGTTCTATATGAAGACAAAC AGGTGGCCATACCTGGGTGGAGGATACCGCTGCTATTTCCAGATTCJAGATTTGGTGAAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCAAAAACAGAGGTATGA
WI-9557	74 C	T ---		---	AAAAGCTTTAAAAAAAAGTGGTGTCTCTTTAGAAACACTTTTCAGCAAGATCAAGTAGCCACGCT ACAGCCTCTGGTGCATCTTAACCCCTCTCCTTT

WI-9617	37 G T	---	---	TGCTCTTTTATTACGTTTCACACACACGCCGTG[GT]GGCAGCTACCAAGTGCCCGCAG CGCCACGCTTGGCCGGAAGGTCTCATTCTGTCTCTATGGAGTATTGAATTTGGGATGGCCAG CTCAGAAATGTTCCACGTGGGGGCACTCTGTGGCAGAGAGGCTGAGCCCTTGCCACACTGGCACCA AAGAGTTGCACGATGCAGTTGCAGTGGTCCAGCCGGGTGTCTGTG
WI-9657	121 T G	---	---	AATGCTGGAGAAAACATCAACATTGAGTTGACATTGTTTTGCTGAAGTATAGCTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAAGCCAGATTCTCAAAATAAAGT[GT]GATAATTCTT TGATTAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAATTAATGCTTTTGATATAGATTGAGG
WI-13119b	114 G C	CCTCCCAAGTA GCTGGGA	AAAAATTAAC CAGGTGTGGTG T	CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGATGT[GT]CACCCACACACCTGGTTAA TTTTTTAAATTTTGTAAAGATAGGCTCCTACTATGTTGCCCGCTCTCAAAAAACAAACCAACTAAC CAGGGCTTGCTCTGCTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT[GT]GACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGATGTGACACACACACCTGGTTA ATTTTTTAAATTTTGTAAAGATAGGCTCCTACTATGTTGCCCGCTCTCAAAAAACAAACCAACTAA C
WI-13119a	51 C G	---	---	ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT[CT]CTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAAGAAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACCTATGTCACAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-13112	71 C T	TCATAAAGAC TACAGACTTA AGCTTTT	TTAGAAATTTT GTGTATTATAT GGAAAAAG	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA[GT]AACAGCATCAGTAGGTACACITTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAGAAAGCCCAAGGTGAGAGTATAATGAAATATGTACAT CTTTATGAAACTGTTTGTGTGACCATCTTTATCTTCCCTGTGGATGAGATGTATGCACACACAAGT AAA
WI-12988	36 C A	CTCAGTACAA GTTT	CAAAGGTACA CTACTGATGCT GTTT	TGCTATTTCATGACAGACACGTGAGACAAATATTCTTATTTTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGAACCTGAGACTTT[GT]ATCTGCAAAAGGGTTTAAATAAT GCAATATCACATATAATTTCCATTTTAAACACCATAATTAAGTTTCCATTTCTTAATAGAAAAATGA TAAAAATGTTTCCCAATAT
WI-13020a	108 G A	CTAATAGTGG AACCCTGAGA CTTT	CATTATTAAAC CCTTTGCAGA	TGTATAAAAAATCCAACTGTTCCACAAGTACATATGCTCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAGTCC[GT]TACAAAAAACAAGCATTTCTCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAAATGAGATTGCACACTAAGCGGATGAGGCAGAAAGCA AGTTGTGTC
WI-12837	87 A G	CCATATACAT ATATCAAGGT AAAGTCCA	GCCATAGGAA ATGCTGTTTTT	AGTTGTGTC

L42611b	50	G C ---				GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCTGTGTCGTCCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCAGCTTCTCTCTGTCTATACCT GCCCATCTGAGCACCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATAATGTATTCAACCA CTGGAGCTTCACITTTGTAC
L42611	34	T C ---				GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCTGTGTCGTCCTCCTGGCCTCTAG TCTTCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCAGCTTCTCTCTGTCTATACCT GCCCATCTGAGCACCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATAATGTATTCAACCA CTGGAGCTTCACITTTGTAC
WI-1172b	179	C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG		TGAACGTGTGGTTAAACCTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCTTTC AAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGACAGTGAAATAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17	C A ---				TGAACGTGTGGTTAAAC[C/A]TAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCTAGAAACA GTGACCACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAATACCATTTTCTGCT TTCAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGACAGTGAAATAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35	G C A	GCAGATTGGA AGTGTGAAAA	CACTTACATTT CTGAATATTTA GACTCTTT		AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTGAG AAATGTAAGTGTGCTGCCCTCACTGTTCTTTACCCACTTAATTTCTGCAATTTTGAAGAACTAGATTGAAT TCCCTTGCAAAACCCCTTGCAATGATGATACCCGAGTTAAACCGTTAATTAAGAGACATTAAACATGG CCTGGTG
WI-1231b	141	G A ---				TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATT CAACTAAGCAGGAGTGTACAAATAAACAAACATAGGCTCTTTATTTCTCCCTTCTTTCAATTTTCTT TCAC[G/A]TTATCCCTCACCTGAACGCCCTTCTTCTCGTAGTGACATTTTAAATCCACTTTAC ACATTCGGACC
WI-1231a	126	T C A	GGCTCTTTAT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA		TCCATGGTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCCACTATGCATTGGAACATTCCCATATT CAACTAAGCAGGAGTGTACAAATAAACAAACATAGGCTCTTTATTTCTCCCTTCTTTCAATTTT CTTTCACGTTATCCCTCACCTGAACGCCCTTCTTCTCGTAGTGACATTTTAAATCCACTTTACA CATTCGGACC
WI-472	114	G C ACAGAAAAAG	ACATACATAT CCATTATACA	GACCTTCTTT TCCAGGCC		GAAGGCAGGAGTGTGTTTGGAGGACAAAAAGTAAATCTTTTATATCTTTATTTTAAATTTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACAAACAGAAAAAG[G/C]GGGCTGGAAGAAAG GTCAAGTGAGATTTCAGATATTTCTTAATGCAAGGCTGACAAATTTGGGCTTGATT

WI-478	46	C T T G T T C	GCATGCTGTG T T A C T C T A T T T	AAATGCCACAG G T G G C T	AAACCACTGCAACCTTCAAGCATGTCTGTGTTACTCTATTTTGTTC[CTAGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATCTCTTTAAACACAAATAGAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAGGCTACCATCAGTACCTTAGCACATTTTAAAAAATAAAAAACCAAC ACTGCCCA
WI-533	29	T C A A C T	ATCAGACAG A G T A C C T T T C T	CCTTCCAACCT C T A C A C A A T C T	AGCCATCACAGCAGAGTACCTTTCTAACTT[CJATAAGATTGTGTAGAGTTGGAAGGAGGACACAGGA CTGTCTGTGGTATATGACCCCTGTGTCCAGTTAATCCA
WI-601b	112	T A ---		---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAGCGAACAGAGAGGTTTCACTGACTCCTAACTGAGTAC[T/A]CAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74	C T ---		---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAAATGATCAATTTCAAATAAAGATGG TAGTGAG[C/T]GAACAGAGAGGTTTCACTGACTCCTAACTGAGTACTCAAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107	A G C C T C A C C A	CTCCTTCACAA C C T C A C C A	CTTCCCGGTAA G C C A A G T	AACAAAACAGACACCCCTCGGCTTCTCTCACAGTCACATGGTGCCAAACAATCCCACATTCCT ACATCCTCCCACTGGCTGCTCTTCAACAACCTCACCA[A/G]ACTTGGCTTACC GGGAAGCATAAA GCCAAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36	G A C	ACTGCTTGCTT G T T G A T T T A A T	TTATTCTAATC C C A C A T G A C A G	ACTCACTGCTGCTTGTGTTGATTAAATCAACCTAGCC[G/A]GCTGTGATGGGATTAGATAAAATA AACACAAAATGAAAACACACAGATTGCTAACAAAGCAGATCTTTTTTCAAGGCACACGTAAGAT AATAACTTCAA
WI-991	37	A T ---		---	TGCATTCATTATGCACCAATAATAACTTCTGTACAT[A/T]CATTATTGATTTCATTATCACAAAAT TATGAGTGAGGGATGATTGTTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCAAAGTCACAAAGTTAGTGACAGAGCGGGATTCCGAATCCATCAACTTGAATCCAGAGAAAAT GTTCTGCATCACTGTACAAACACTGACTCCTTTTCTCCTTTGAAAACAAGGC
WI-1011	70	G C C A	CAGTATCTGA A G T T T T G T C T	AGGAACACCTA C A A A A T G A C T T	CTTCTGACCTGTTTGCAGTGGATGTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTTTGTCTCC A[G/C]JAGAAGTCATTTTGTAGGTGTTCTCGGGGTTTTTGCTACGTTTTCCATTTCTCTAATACACTGC CGTCTTAAGGGAGGGCTTGACAGCATTTATCAGATGGCTGTTTGTCTGCACTGTGCACTGAAG
WI-5381	178	A T ---		---	TTATGTCAGAAAGGTCCATGAGTTTACAGAACTCAAGGAAGAAAGGCCCTTAGAGATGACACCAGAA ATGAGAGTGGCTTGCTCATGAAAATTGGACAGCATGTTCCAAAGCAGGGAACAGCATGGAGAAGA AAAATCATACTCTATCCACGTGCAGAAACTGGCAATTAGTTTGT[A/T]TACTAAAACACAAATGT TTAACTTGGGGTCCACAAACAAGGATATGTTGGCAATGGTATTCTGTGATG
WI-5791b	76	G A ---		---	CTATGATTCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCAAAAAGATGAGAACAGGTCTTA GAACCTCAG[G/A]ATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCCAAGGTA AAAAAATAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTCTTATTTTGCCACCCTGTTTGT TAGGAA

WI-5791a	44 C G ---			CTATGATTCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTC/GJACAAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCCAAAAGGTA AAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTGGCCACCCTGTTTGT TAGGAA
WI-5406c	120 C T ---			CACTCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACC/CJTJATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGGAAAGAGAGGCAAA GG
WI-5406b	118 C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT	CACTCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACC/CJTJATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGGAAAGAGAGGCAAA GG
WI-5406a	42 A G ---			CACTCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGGAGCCACTTCCACAGATGCAACAG GCCCTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGGACTCTGTGAAGAGGAAAGGAAAGGAAAGAGAGGCAAA GG
WI-5798	48 G C TG	TTTATTCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAGTATTT TCAAT	CCATTCTCTTCTCCCTCTCCCTTTATTCTCCCTTGTTTCTTTTG/GJATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACATGTTAATCAATGCATAGTTCTATATGGGTATCA
WI-5415	54 T A TTT	TCCTCATGAAT TCATCTTTCAG	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTTAAGCAGGATTTGTCTTCATGAATTCATCTTTCAGTTT/AJTAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41 C T G	TCCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGCAGACCTCCAGAGAAAAATCCAAGAG/CJTJTTAAACCATAATTTTGTGTTTA GAACTCCTGTGCGCAACCACCTCTTGATGTGAGTGAC
WI-5481b	131 A G CTGAGTCG	TGTCATTTATG	TTACTCCAGG CTCCAAGTATT	AAGCCAAATTCACATTAGTTGATGAATTTGAATTTACAGTATCTAATGCATGGGCATCTGTTCAAC TCTGTGTTTTCAAGAGGAGTAGTATGTCTGAAAAATCTATTTGTCAATTTATGCTGCAGTCG/A/GJA ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5481a	29 G A AATTT	CCAATTTAC ATTAGTTGATG	CCCATGCAITTA GATACTGTAAA ATT	AAGCCAAATTCACATTAGTTGATGAATTTGAATTTACAGTATCTAATGCATGGGCATCTGTTTC AACTCTCTGTTTTCAAGAGGAGTAGTATGTCTGAAAAATCTATTTGTCAATTTATGCTGCAGTCGAA ATACTTGGAGCCTGGAAGTAAAGACTTGGCTATTTTCACAATTA
WI-5492	38 T C ---			TCATGAGTCTTTCTTCAAGAGATGCTTGTAAAGTCCCA/TGJCAAGAAAGGATCCCATGGCCTAAT GAAGATGTAACCTCCACCTTAGGATATTTTGCAGACCAA

WI-5826	134	T C	---	CCCAATACITTT TTCAGGTGAA	---	TATTTTTTTTCTCAATTCCTGGAGCACACCATGCTCTTTCTATTTCATGCTTCACATTTATTTTTT TTTCACTTAGTTAAATGCTTTTCCCTTGATCTAGCAATGCCAGTTTATACATATTTCTTTAGT[C] TTTCAATTAATGCCACCATAGAAATAATTTCTAACCAACAGCCAAACAGCCTCACTCTTCCTT CCTTGGTGCAITTTACTCTTTACAC
WI-5546	40	C T A	GGCACCAGCCT TTTTAGAGT	CCTGTATTTTA GCAACATGGG	---	CCTTATAACCCCAATACITTTTCAGGTGAAAAAGGGAAAA[C]TACCCTAGTTTCTGCTAAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATACAAATGCTTGAGTGTAATCTGATGTGGGAATAT TAGAAAAATTAAGCGAGAGAGGCA
WI-5552	97	C T	GGCACCAGCCT TTTTAGAGT	TGCACAAATTG CCAGG	---	TGTTTGTCTGCACCTCCCAACAAAGTGGTCAATGAGCCTCAAGGTTTTGATTGAGCGGGTATGGGT GGGGCTATCGGCACCAAGCCTTTTAGAGT[C]TCTGGGCAATTTGTGCACTAGTGTGAGA
WI-5836b	161	C T	---	---	---	TAAAGTGATTTAAACACTCTGTGCTCAATTTTTCACCTATAAAAAAAGATAAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAGGTGGATAGACATACTCTGATGATACTGTTGTATCCCTGAA TCCTGCAATATACACATGATTCATGAT[C]TCCCATTTGAAAAATTAAAGCTTTTGAATTGTTTTTCCA ATG
WI-5573	58	C T	GTTCAAGG AGGTGGGA	TGAACAGTTGG AGAGTAATGTG TC	---	TCGGGTATTAGGATGCGTTCAACCTCGATGATGGGCGTTCAAGAGGTGGGA[C]TGGACAC ATTACTCTCAACTGTTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G A	---	---	---	CAGGACCTTGGAGCCTTGTCTGTTTGTCTTCCACCCCTCACTCTTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCCCTATGACGCGTCTATCTCTATATGGGGCAATATCCAATGTCCCATTC[G/A] TTTTGGCAITTCCTGTATATCAACAGAGAGAGAGGTTGG
WI-5850a	92	C T	---	---	---	CAGGACCTTGGAGCCTTGTCTGTTTGTCTTCCACCCCTCACTCTTCTGCTGCCATGGGTGGAGC CTCTCAGGCTTCCCTATGGA[C]TGGCTCTATCTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGAGGTTGG
WI-5612b	125	A T	CTATTAATGA GCATCGTGCA TTC	TTCTCTTGAGA AACCTAAAC ACTG	---	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATCTAACATCACAATAATCTTATTTCTGCCTG TCACACTAATTTGCAAGCATTCAATTGATTGACTATTAAATGAGCATCGTGTCAATTCAT[C]TCAAGTGT TTAGGTTTCTCAAGAGAAATTTATGCTGTTCTTCTGTAACCTCAAGTA
WI-5612a	44	T A	---	---	---	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATCTAACATTCACAAAAATCTTATTTCTGCG CTGTACACTAATTTGCAAGCATTCAATTGATTGACTATTAAATGAGCATCGTGTCAATTCACAGTGT TTAGGTTTCTCAAGAGAAATTTATGCTGTTCTTCTGTAACCTCAAGTA
WI-5636	26	A C	GCCAAATTTAT CCGCAATAAA	CATCGAGGACT TTGGGA	---	TGAGAGCCCAATTTTATCCGCAATAAA[C]TTCCTCAAGCTCGATGGAGGCAATTCAGAAATCGGG GCAGGGGAGGCAAGGTGAGACAGATGTGAAGAAC

WI-5865c	103	C G ---			---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTATGCATTC ACTGACTCACTCACTTGCTCTATCAAAAATTAAAC/GIAAATATTAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA GAGAAGACAGACAACATAAATAATCCAGG
WI-5865b	99	T A ---			---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTATGCATTC ACTGACTCACTCACTTGCTCTATCAAAAATTAAACAAATATTAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTTCA GAGAAGACAGACAACATAAATAATCCAGG
WI-5865	165	T A ---			---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGATCTTTTTTTCATTATGCATTC ACTGACTCACTCACTTGCTCTATCAAAAATTAAACAAATATTAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAATGACCAAGACACAGTAAACAGTCTCCATCTTCAAAAGGTCACAGTCTTCC AGAGAAGACAGACAACATAAATAATCCAGG
WI-5874	76	T G ACAGAAAA	CATAGCATGG ATAATATTAT ACAGAAAA	CCTAGTAAGTT TCAGTCATTGG ATATGT		CTCAGACATTCATTTTCATTAGTTGTTAATTTTGTGTTATTTTCATAGCATGGATAATATATACAGAA AAAAAATTT/GIATACATATCAAAATGACTGAAACTTACTAGGTAGCAATTTGTTTGCAATTTGCT CATGGAGCCGACGTTTCAGCTCTCAGTTTTTCCATC/A/TTTTTTTCATAATTTACTCTCTTTTCTGTC ACAATGTTCTGCTTCGTATTTCACCTCATTGCTGATTGGATGGTAGTCATAAAATATGGGTGATTTC AGAAAAATAAGTAAATG
WI-5752	36	A T TTTTCCATC	CAGCCTCTCAG AGAGTAAATT ATGAAAAA			TTAGCAGAAAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCGATAAAATAC/GJC CATTAGGTATTAGATAAGCATCCCATAAAAACATTGTTGAAAAACGAAGCCGAGTTTCGATTTCACACA GTTGCTGTTTTAACCTCTCTAAATCCCGATAAAATAGOCATTAGGTATTAGATAAGCGTCCCACGAAA CATTGTTGAAAAACGAAGCCACGTTTTCCGATTTCACACAGTTAGTTGCTGTT
WI-5760b	61	C G ---			---	TTAGCAGAAAAACAACAAAAATGTCACAACACTGCAGTAAAGAGTGTTCCTCGATAAAATACCCAT TAGGTATTAGATAAGCATCCCATAAAAACATTGTTGAAAAACGAAGCCGAGTTTCGATTTCACACAGTT GTCTGTTTTAACCTCTCTAAATCCCGATAAAATAGCCATTAGGTATTAGATAAGCG/GA/TCCCACGAA ACATTGTTGAAAAACGAAGCCACGTTTTCCGATTTCACACAGTTAGTTGCTGTT
WI-5760	187	G A ---			---	AATATCTGGCCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTTG/GA/GTGAAGTTAGAT CCCACCTCACTATTGAGAAGCTAAAGGTGAAGACTACTCATTTCTCAGICTTCTCTGCTG
WI-5944	52	A G GGAATCTTG	TTCTCACCATG AAGTAACTTG	GGGTGGGATCT AACTTGCA		GAGTTTAATGAATCCTGTTCCCTCTAAAAACCTCTCTGTTCCCACTTCACATTTCAGCAGATATT CTTTCATGGGTTATTTGCCCCAAGTCATGAGGAGATGCATGTAATTTGATCATTTCAAGAGTGTGAG TAATGCTTGGTA/C/TJTTGCTCTGTGCCGTATCTGCTCCCAATCACCCATTCCACTTTTATTTCTTATTAT GCTGAATGAAACGGTTATATACAG
WI-5967b	148	C T ---			---	

WI-9720a	47 A G ---	---	CCTCTAACAAAGAAACCTTGACTTCCTCAACTCAAAATACCCCTCTCTA/GJATAATTTAAGTAACCA AAATATTCCTTCAAATAAATTAATCTTTAATTAGAAGAACCAACAGTGTTAGAGGTAGTACATTCA CCACC
WI-9825	123 A T ---	---	CACGCTCTAAGCAGGATGTGGCTTATGAGATACTTGCATTGTCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTCATGTCAGATGAAGGCTCAGGGTCTA/TJGAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTTACAAGAAGAACTCACCAGGGTTAGTTGCATT TAAGAAATGCCAGTCTTTTGCTGCTGCATCATCTTGAACATTATCCACATG
WI-9748	74 C G ---	---	CCACTTCAGTAAATCAATTTGTAGCACCTTATTTCTAAAGATTCTAAATTTTATATGTTTACCCTTT GTCATT/C/GJTCAGACCAAGTACATGTTTTCACACAGCCATCTTTCTTCTGGAATCTTTTCAGAAT TACAGTTATGATGTCCTTTTATATTCGCCA
WI-9943	91 T C ---	---	TGAGGCTATGATTGCAGATTGTAGTGACTAATACTATTAAAGCAATTTCAATGTTGTGGGCACGTGT CGTTGTGTTTATATCCATCTT/CJATTTTAAATTTCTACTGAGCAGAAATAAATGTATACATT AACCTTTGCTCCCTATTGTACCTTTAATATGCAATTCACACCTTCTCTTTTGTCAATTTAGGGA
WI-9891	39 T C ---	---	AGGGCCCTTCACAGATCCGTCAGCTCAACACTGCCTCCTT/CJAGTGAGCCTGTGAACCCACCCAGAC GGCTGGTCATCAGTGTATCCTCTCTTCCGGACAACTATCTTTAAAGAAATAAAGAGAGTGT CTTTGAATGTATCCATTTATCCCCAAATAATCTTGTTTAAATAATCCTTATTAGGCCAAATCCAAAT GTGCTGAAATATCTGCCAAGCATGTCAATCTACACAAAAGGGATTTCGAAA
WI-9897b	84 C T ---	---	CTCAGAAATATTCAGATCTCCCCAAATGTCATGATTCTTGTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGT/CJJAAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83 A T ---	---	CTCAGAAATATTCAGATCTCCCCAAATGTCATGATTCTTGTCTCAACATCCTATTTTCTCTCAAAC ATTTATCTAGCCTGT/CJJAAGTCATCCAGTGAGGCTGTTTATTCATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115 C A ---	---	AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGCACACCTCACCAGAACTGGAAGGAGT CTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTTCAGACA/CJAJGCCAAGAAAAGCC TGATATTAGAGGCACCTTGCAATTA
WI-9935a	42 C T ---	---	AGATAACCCCTGGAAAACCTAGAAGAAATTAATAACGTGTTGCAC/CJACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTTCAGACACAGCCAAAGAAAAGCC TGATATTAGAGGCACCTTGCAATTA
WI-9983	146 C T ---	---	CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCCTCCCAATTCCTTTGTCTTGA TTCCCCAAACCCCAAGTTCTCACCCCAATCTGATCAAAATGCTGACTAGGTGCTGGCTGAGGTTAA AGCATTTATGA/CJ/JAGACACAAAGACAAAGAGGTTAAAGTTGCTGTCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACTAAGTAAGGCTTCGAGGAGGAGGTGAGCAAAGG

WI-10019	139	A T	TGATGTAATGC TATGTAGCAA ATCT	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGGTTGAGTATACAGCAATCTATTTTGTATTATTTATGTGTGCTATAAATCAATGGTTCTA ACATTCAATAAGATCTTTTGTCTCTGCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAAAT CTA/TATCCCTTAAGCACAGTAAATCAAGGCCCTTCTACCCCA
WI-10020b	122	T A TTT	GCGAGAAAAG AAATCATGAC TTT	GACTGTTAATT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAAATTTAGGC ATGCATAGAGAAATAGCAGTGTATTTTATGGCGAGAAAAGAAATCATGACTTTTTT/AJAAAAATACC AGACTAATGATTAAATAAATAAACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
WI-10020a	39	T C A TAAAT	TGTCATCTGA CTCGATTAA ATAAAT	AAATTCCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAATTATGTTAACTGGCTCTGAAAAGAAATTTA GGCATGCATAGAGAAATAGCAGTGTATTTTATGGCGAGAAAAGAAATCATGACTTTTTTAAAAATACC AGACTAATGATTAAATAAATAAACAGTCTAGGGTTCCGGAAGTGGCCTAAAGCACGTAGTAGCCCT CCTTAGA
WI-10064b	170	C T TTTACATG	CCTTAGATAT ATTGTGATTGT TTTACATG	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGGCATTATAATAAAT ATAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGTGGTGACACTCTGTTTATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATG/C/TJGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10064a	54	C A CAGGGAAGG	GTAGCAGGAT CAGGGAAGG	GAGATGCTCTG CAAATTATATT TATTAT	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAG/C/AJATTATAATA AATAAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGTGGTGACACTCTGTTTATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAGGTTAGGTGTT T
WI-10289	29	T C CAAACTCTT	TCTCCTGTCCC CAAACTCTT	ATTCITGTTGT ATTGAATGGAA TTAA	CCAGGGATTCTCCTGTCCCCAAACTCTTA/T/CJTAAATCCATTCAATACAAAGAATTTATAGAA TATGCACCACATGCCACAAAGACACCCCTTATATTAGT
WI-1319	40	A T ATTCTTT	TGGCACTTAG AACATAGTTT ATTCTTT	GCCACACACCC CTATGGT	AAGAAAATCCTTGTGGCACTTAGAACATAGTTTATTCTTTT/AJACCATAGGGGTGTGGCTTATCT TTTACCTGGCATGGCTTTAGGTCCTGTTTATAAATTTGGTATCTTTTGGCACAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTTAAACATTAACTGGTCAGATGTTTAAACITGTTGAACCTGCAGC
WI-10316	104	T C CTCTT	CTGTTGATTTT CTACCTCTATT CTCTT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACITTAGTGAGGTGTAATCAGAAGCATCTATATTATTCACCAGTCACCACCCTG GACTATAGTCTGTTGATTTTCTACCTCTATTCTTAT/CJTAAACTTTTGGATACATTCCAAAGCAT CATGGTCACTTCCAGTTATGAAGGATGTTTAAAGCCCGCC
WI-2572	61	C T	AGTGAGTTGTCACAATTTGGAGACATCTGTGACCCCAACTTAAACACATCTCTCCACAC/C/TAC AAAGTTAACACTTCAGTTACCAGGTGATTGAGCAGA

WI-10368	31 C T	TGAAGCAACC AGTCTTGT	CAAGATATTAT ATTTATTCTCT AAGAGGGG	GAGGAAGCTGCCTGAAGCAACCAAGGCTGTGTTC[C/T]CTACCCCTCTAGAGAAATAAATAATATCTT GAGATAGGGAGGAGCAGCCTGAGGACAGCTGGGTTTGTCTACCCCACTGGAAGCAGAATATCC TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAAACTATATGACCCTGATGGATTGCCTTTACGGG
WI-10391	32 A G	CTGTCTCAGGT ATGACTCCCA	GGGAGTTAGGA GTCAAGAAGTT GA	CTCTCCGTTCTCTGTCTCAGGTATGACTCCCA[A/G]TCAACTTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTCCAGGGGAGCATCTGACACAGCCTTTTGCTTGCTGTGACAAACAGAACATTTGCAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146 A C	GTTACCCAGA GTCCTCTAATA	TGCCGCTTCCA GTAGCT	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTCTCAATAAATATTATCTTTTTCATATT TTCCAAATTTAATACTAGAAATTTTCAACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGCTT CTAATAGCAA[A/C]AGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567b	82 A C	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTCTCAATAAATATTATCTTTTTCATATT TTCCAAATTTAATACTAGAAATTTTCAACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAG TCTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-10567a	60 T C	GGTGCTCAAT AAATATTATT CTTTT	AAATTTCTGTT GGTGAAATTTT TAG	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTCTCAATAAATATTATCTTTT[C/T]CAT ATTTTCCAATTTAATACTAGAAATTTTCAACCAACAGAAATTTTAAACATTTTAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAACCCCT
WI-11153b	84 C G	CAAACTCAA ATTGCTTTAAG TACTTTA	AAATCCAACA GTCAAGGTCTT C	CGTTGGGAATATTTCTATCTCACCTAAATTTATGCGTGATTAATAATATACATTTTAACAAACTTCAAA TTGCTTTAAGTACTTTA[C/G]GAGGACCTTGACTGTTGGATTTTGAATTTTCTTTTATTTCTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33 C A	GGGAATATTTC TATCTCACCTA AATTATG	GCAATTTGAAG TTTGTTAAAT GTAT	CGTTGGGAATATTTCTATCTCACCTAAATTTATG[C/A]GTGATTAATAATATACATTTTAACAAACTTC AAATGCTTTAAGTACTTTACGAAGACCTTGACTGTTGGATTTTGAATTTTCTTTTATTTCTTAATA AAACATGCATATTTAAGTTGTCAGCAAGATGTACTTATATGTTAATTATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125 T C	CACAAATGTA ACAAGAATTG ATCC	CCATGGCTGTA GTCCAGT	GTTGTGAAACTCCAGTATCATTTCCCTCAAAACACGCTTAAATCACAATCAGCTTTTCTTTCTGTA GAGCTCAAACTCAGTCTGAATGAAATGCTGCACAAATGTAACAAGAAATGATCCTA[T/C]ACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58 C T	CAAGTGAATT ATGACCAAAA TGAGA	TGCTCTTTCA TTTGAGGTTTT T	TGACTCAAAAGGAAACACACACAAAAAGTTTCAACCAAGTGAATATGACCAAAATGAGA[C/T]AAAT TTGTTAAAAAAAACCTCAAAATGAAAGAGACAAATATAGTTCAAGATTCAGGTTCAATATTTGT ACCTACAAAATAGGGATAGTCATGGTGTGGCAGACTTTTCTTTTCTTTTCTTTTCTTTTCTTTA GAAATCCATTTGCTTTTGGCCAGCAATCCCTCTCCCATATTTTAAAGGAGAGAAATTCACCTTTTCT CTGTTGGATGATCACAGGTTCTGCTCTTCCCAATCCAGAGGAGGAGTACTATTACCCCATGGGTCAT AGAGAGGATTAAACAGGGGTGATGCCTGCAATGGGAATATTGAAAAACC
WI-10656	59 T G	

WI-11169b	154	T G T T T T	TTAACCAAGA GTTTTTCATTG	CTAACTTAAA ATCCTCATTCA AAATATAA	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATAAAGCTAAAGTAGTGCTTTTAAACCAAGAGTTTTTCATCTTTT TTTAAAAAAGAGCAGACAT/GJT/TATCATGTGTTCTGATAATTTTATATTTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95	A G T T G A A A A A	AATAAGTGAA AGTAACTGAC	AAACTCTTGGT TAAAAAGCAC TACTT	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTTTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATAAAGCT/GJ/AGAGTAGTGCTTTTAAACCAAGAGTTTTTCATCTT TTTTTTAAAAAAGAGCAGACATTTTATCATGTGTTCTGATAATTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25	A G ---		---	CAAGTCTTGGACCTTGGATAGGTG/JG/JACCGGCTGAAGTTGGACAGTTGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTTGTCTCTTTGGGTTTACCCTAGGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTTGTCTAAATAATTCAAAATAGCCATGGGTTTGGACAAAATAC AAGGTAGTGTCTCTAACTTTAATGGGCATA
WI-10686	133	C T A A G G	TGCCCCGTGTC T A A G G	CAATCTCTAAA TTCATGTGTAG ACACA	AATAACCTGTGGCACATAAGGCAATACTGAGCCCCATACAGAGTGTTTATGTATAATTATGAAA AAAGTCAAGAGAACAGATAGTATAGTCTGCTAGATACTTGAATCTGATGCCCTGTCCAAAGG C/TJTGCTCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAGGG
WI-11175	77	T A A	AAATGATTCTT TCTGCTCAAAG	CTGTTCTCACA TCTTTTTTGAA AA	GGTAGGATGATCTAGAAATGCCACTTTACAGCCACTGAATATATGCTCCCAATGATCTTTCTG CTCAAAGAGT/AJTTTTTTTAAAGTTATCTACTTATTTATCTGCTTTTCAAAGAAATGTGAGA ACAGTACAAAATGTGTTTCAGTATAGCAAATTAATAATTAATAAGTAAGAAAAAGAACCAATT TGGGC
WI-10694	144	A G T A T G A G T T T C	TGCAAAATGCTT TATGAGTTTC	GGCATTTTGTA AAGGAGGAA	TAGAGAGGCTTTTCAGTTTCAGGTTGGAGGGTGGTGAGGTTGAGATTCCTTTAGAGCACTGGC TATGTACAGAAAGATAAACTCTGAGAAAGAACTCAGTTCTAAAGTTTCAAGTCTTTGCAAATGCTTTA TGAGTTTTTC/JG/JTTTCTCTCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAAAGCTTTCT
WI-2716	23	T C C	TGAATTCATCC AGAAAAACAG	TCTCTTTTCTC TCTTGTGTCA TTC	GTGAATTCATCCAGAAAAACAGCT/CJGAATGACAACAAGAGAGAAAAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTGTGTCCTCCAGTGCATGGAGCAGTG
WI-10719	115	T C G C C A T T C A G	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC	CAGGCCCCAAGCTGTGTCATTAAAGTTTGAACACAGACACCTCAGTCACACAAAGTTTCTTGTATGT GCCCCACCAATAACAGTTACTGGAGGATGACTCTCAAGGCCATTCTAGT/CJGGCTGCTGGCAGTCTT TTCAGGCTGTGCCCATAACTAA
WI-10721	40	A G C T T G C C A	TGGCTCTGCTA CTTGCCA	GAACTOCCAC ATAAATAAAT CTCA	CAACCAATTGAGATTTAATTTTGGCTCTGCTACTTGCCCA/JATGAGATTTATTTATGTGGGAGTT TCTGAAGATTCCCATGGTAAATAGTATTCCTCTCTCCCTGCTTAGGTTTTGAAGAAGTTGAA

WI-11204b	88 T C ---			GCACACGAAATTGATTAATATTGGCTGACITTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTTTACCTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTTAGTGAATCAGAAAAATAAGTCTGAGGAAATTTATTCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAGGG TGAAAAGAAA AATGTACATAA TACCTTT	--- TGATCACTTAA AATGTACATAA TACCTTT	GCACACGAAATTGATTAATATTGGCTGACITTTGAGGAGGAGAACAGGGAGTTGAGGTAAAAAGGGTG AAAAGAAAAACTTTT/CJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTTAAATTTGGGAAGAGATTTAGTGAATCAGAAAAATAAGTCTGAGGAAATTTATTCAGAAG GCAACATC
WI-10732	80 C A ATTGGTTCAC	GCTGTGTCTTC CTGTATGTACA CTGTATGTACA	AAGAACAATG CATAACAGAA CTTTAA	ACATGTATTTCTTTAGTGTGTCAGCCTTCTTACCCCCAAGAATATCCCTGGITTTATTGCTGTCTTC ATTGGTTCACIT/CJATTTAAAGTTCTGTATGCATTTGTTCTTGAGTCCACATAGGTGTTAATCATTCCA CACCACCTCTGTTTAAACTGTC
WI-11206	127 A T ACTC	GGTTGTGTTTT CTGTATGTACA CTGTATGTACA	GAGTGACAATC CTAATGGTTGG	TAGTCTTTTCTTTGTACGAGTGTCTATAAAGAATTACCCACTCTGTACATTTTGTAAAAGATAGCACAG AGAGAAGCATTACAGGGCACACACAAACATGAGGTGTGTTTCTGTATGTACAACCTC/JATCCAA CCATTAGGATTGTCACCTCTCATATATAGACAGAATTCAGTGGTGGTGAATTTGAATTCACACACATGGA ATAAGTCTA
WI-11215	68 C T ---		---	GAAAAAAGTTTAAATGGATTGCTTAGTTGCTTAAATTTGACCTACITTTACAGATTTATTTTAGT [C/JATTTTCTCTATAATAATTTCTGTAGTGATGGATTTCTATAAATTAAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTCTTTATCCAAAGCCCCATTCACCATGT TTT
WI-11219b	89 G A AGAGAAA	GAGAGAAAT TCCAAAAAGT	GGTCTCTAAT TTTTCTACACT TTCT	ATGAAAAATGCATTAGAAGAAATTGGAGGATAAAAATTGAGAGAATATTCAAAAAGTAGAGAAAA GAGACAAAGAGATGAAAAATAGGA[G/AJAGAAAGTGTAGAAAAATTAAGGAGCCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11219a	18 G A ---		---	ATGAAAAATGCATTAGAA[G/AJAAATTGGAGGATAAAAATTGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAAAGTGTAGAAAAATTAAGGAGCCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11222b	136 G A GCGTGG	CATACCCTGC GCGTGG	CCTGGTAGCCA AGTTGTGA	AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAAAATGCTAAAAATTTGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCCGTTGAACATTTGTTAAACATTTACCAGCATACCAGCTGGCGCTG G[G/AJTCACAACCTTGGCTACCGAGGAGAACCTGACACAGACTTCGTAATTTGCTTTACAGGCTACTGG AAAGCC

WI-11222a	25 C T A	GCCACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTCG	AGCCACAGTGGAAATCATTTACACTA[C]TCGAAATCAGCAATGCTAAATTTGGGGCTTTGGATTTT TGTTTTGTTTTTCCATAGACCCACCGTTTGAACATTTGTTAAACATTTACCAGCATACCACGCGG CTGGGTACAACTTGGCTACAGGAGAACCTGACACAGACTTGTGAATTCGTTTACAGGCTACTGGA AAGCC
WI-10775	39 C T	TTTATGOCATA TTAATTCATTA CACTC	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTATGCCATATTAAATTCATTACACTC[C]TACATCATATTTCTTAGCAATACA TCTAGACACCTGGCACTCAGTAAGGATATTCCTGGCAGATAATCATTTGTTATCATTAGACATTGCA GGAACCCCATATGGATGATAAATGTTGTTTAAATGAAGGCAAGCAATTA TTGCATGCATTTATACGAAAGGAATTAATAATATCTTCTTATAGTTGAATTTAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATAGAAAAATGTCAGTGGTTGC TAGTACAGGAATCAAATTTGGACTATGAACA[A/C]GACATAGTTGCTAAGGATATTCACAAATAT TTCATGA
WI-11226	165 A C	---	---	CAGTGGCTGGCTACTGACAAAAACGTAAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG[A/G]G TCCATCTCTGATGTACCCAGCAGGGCCAGGAGGTTGATCTGGAG TGGGACACACTGCTCTAGACC[C]TTCOCAGGTCCTCAAAGTGGGTAGAGGCCCTACTGCCCT GCCCTGGGACGACAGGATCAGGGCCTTAGTCTCTCTGGGACAGTGAAGGGCCACCAOC ACAGAAAAATGCCTAGGCTTGTAGCAAGAGAGGAAAGCATCTTCATGGGCGGAAATTC[C]TTCATTT CTGTGTTCTTAGGGTTTGTGGCTGGCCATCAGTTCACTCAGCCCTGTCCTGATCCAGCAACATT TCCGTAACCTACCCCTCTAGAAGTCATGCAAGAGAAATGATGA
WI-10778	62 A G	GCAAGGGAGG AACATTTACA G	CTGGTGACATC AGAGATGGAC TTGAGGGACCC TGGGA	GGACCAACAGAAATTAATCTGGCA[C]CAGGGTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAGGCTATAATTTGGATACATTAGGCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10789	21 C T	GCGCTAGACC	CAAACCCCTAAG AAACACAGAA ATG	TATGCCITCCCACAGGCCATCCACGCTGCTCTTAGCACAAAAAATAGAAATACATCTGAATG GGCACATTAATCTGCAGGCTCTCC[C]GCTTCTAAGTCACCTGCAGTTAGTCTGCAGACACTGTGTA TACCATAAATCTGATTTCTGAGCAGGAGGAGGAGGATGAGAGAAGGGCTGCTCCGTGAAATAC TAGTCCG
WI-10810	58 C T	CATCTTCATGG GCAGGAAT	---	GATTGAGTATTATCAAAATGCCCCAAGACCATTAAACAAGATTTAATAGTTAAAGCCAAACTATA AAGAAATAACTGTTCAAAAGTGTGTTAAT[C]TCTTAATACCAATTTATAGGGCCACCATTAACTT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT GGATGATGTTCTGTGGTCCCTTTAT[C]AAAGCCCTCTGCATCCCCAAATGTGTAAATTTATTCTCT TGGTATTTCTCGCTTACCCTAGTCACTGTCAAGTGTTCACCCCT
WI-10828	23 T C	---	---	---
WI-10832	91 G C	CATTAACTGCG AGGCTCTCC A	CCTAACTGCAG GTGACTTAGAA A	---
WI-10834	96 C T	AGAAATTAAC GTTCAAAAGT GTGTTAAT	TGGCCCTATAA AATTGGTATTA AG	---
WI-2287	24 T C	---	---	---

WI-2906b	77 T A ---			---	CCTGAACACCTGGAGCAGCTCCCTCCCTGGACACCTTCATCTTCTGGAACTTTCCTGGAACTGCTCTTCCCTCTGAGAGCTTGTCTGGCTTACTTTCTTTCTTTAGGTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTTGTGACCAACAAA
WI-2906a	50 A C TCTTGCTGG	GACACCTTCAT		AGAGCATTCCA GGCAAGT	CCTGAACACCTGGAGCAGCTCCCTCCCTGGACACCTTCATCTTCTGGAGACCTTTCCTGGAATGCTCTTTCCCTCTGAGCTTGTCTGGCTTACTTTCTTTCTTTAGGTTTCAGCTTCAAAGTGACCTCCTTAGAGTTGGTTTGTGACCAACAAA
WI-1736	175 C T ---			---	TACTCCTCATTCTCCTATGTCCTAGACGTAAGTTCATGCTCCCTGAAACATTTATTTCTTAATTAGATTTCCACCCCGACACTATTTACACAGAACAGCATGGAGCAGTTTGGAGCTGCTTAGAGAACTTAAAGGACAGTGGTTTCCATCTGTCTTCCA[CT]AGAGATCTAGGGTGTCTTTGGAACCACCTTGG
WI-1851	136 G A GTGTTAAGTA	GCATTGAATT AACTATAGAT		CACTAGCAATG TTAAACTGAAG TTG	AATACCCACGTCCTAACACCATCACACTGATCATCAATCAGGTTTTAACATATTAACTGGGGAGGACACAAACATTTAGACCATAGCATTGAATTAACATATAGATGTGTTAAGTAATTATTAACATGGTACA[G/A]ACAACCTCAGTTTAACATTGCTAGTGATTCATGTGGATACCATGTACCTTCTTACATCATGTGA
WI-3000	62 G A AGAGACCCC	CCCAAAACAC		GCCACTATAGG ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCAGCTGCTTACATCTCTAAATGTGACGACCCCAAAACACAGAGACCCCG[A/TTGAGCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGATAGTAGACACT
WI-1754	177 G A TAGTC	TTTTCTCCCTT CTTAAAGAGA		AAAGTCGAATT GCCTCTGG	ATGGATCTGCTCAATTATAGTCCCAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTTACTTAAGGGTTTAGCAAAATTCACCTGACAAAGAGTAGGTTTACACATTGACCTCATAAAGTGATTTTCTCTTTCTGTGTTTCTCCCTCTTAAAGAGATAGTC[G/A]CCAGAGGCAATTCGACTTTCTGTAGCCACAAGATT
WI-3167	37 T A TAGATTC	AAATTCAACC ACAGATCTAT		TGTGATAGTTT TGAGATGGGTG	ACAACACAGCAAAATTCACACACAGATCTATTAGATTCTT[A]CACCCATCTCAAACATATCACATCAAGAAAGCAAGGAGACATATTACTGGTGAGGAAGGCCAAATTTCAA
WI-3208	140 G A AGATAAAGA	GTGAGTGGGC		TCACTCAAAC AGGCTTGG	CAAGCACACATTCAGGCAGTGGGAGGTAGGGAAGGTGGGCAACTTCGCAGCAGAGAGGAGGAAGAAAGTCAGACCGTTGGTAGGATAAGTGGATCCAAACCCCTTTGTAGGGCAGGTGGTGAGTGGGCAGATAAAGA[G/A]CCAAAGCCCTAGTTTGGTGGACACTGTGGGGATTCAAG
WI-1775	47 C T TTTTCTCTG	CCTGCATGGTC		AGTTGAGATT ATGACAAATGAT GTAAA	ACTCCACCAACAGTTTGTGAGCCAAACCCGTCATGGTCTTTTCTCTG[CT]TTTACATCATTTGTCATAAATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55 G A ACAT	AGCATATTCA TTGATTTCTT		GAGGACTTAA AAGGAGCATTT G	CTGCCCTTTAGATCCAAAGCCAGTTACTCGAGCATATTCATTGATTTCTCTTACAT[G/A]CAAATGCTCTTTTAAAGTCTCAACTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCTCTTAGGACCTTTAAGTCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCTCTTAGGA

WI-3416	33	C T	CCAAGTTGTA GCATTCAGAA GTC	ACGAGCACAA CTACCTCTAAG AG	TCCTGTTCTCTCAAGTTGTAGCATTTCAGAAAGTC/CTCTTAGAGGTAGTTGTCTCGTCTGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACCTCTCCAAACAAAGTGTACCAACAGCATTGTTAAG GAAATGTGCAATGCTTGCTACCTCTGACGACACACATAATTAATCCCATTCCTCTAAAGAGCCAGG TCCTATTCTTACAAACACAGAAATTTAACAAATTTGAAATTCAGCTACTCTCTTAGGCCCATCAGAG AATCT/TAAGATCATGGGAAATTTGATGCCATGTGAATTTGGAGAAACACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTCCAGAGCCATCATCTGTAAAGAC
WI-3453	70	C T	TTCTAGGCC ATCAGAGAA	TCAATTTCCC CATGACTTC	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAACTTAAATCATCAAGTGTGCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCACAGTATTTAATGAGGTGGT/ATGGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474b	109	G A	---	---	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAACTTAAATCATCAAGTGTGCAACTGGTTTGA GTCAGTTTCCCTAAATTTAGCAC/ATGATTTAATGAGGTGGTGGGAGAAAAATGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90	A G	AGTCAGTTTC CTAATTTTAGC AC	CAACCATCAAT TTTCTCCCA	TTTGACCCCATACATGAGAAATAAACCAATAAGAAATGGTGGAAAAATAAACCGGAGAGACCTGGG TTTCTGGATGTC/CT/TTGAGGACAGGGTCACCCAC
WI-3502	79	C T	CCTGGGTTTCT GGATGTC	GGGTGACCCCTG TCCTCA	TCACGGCAAGTTCTGCAGCAGTGTCTTGAACCTCTGCTGTTTCCAGAGTGTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGGATA TAAACATCT/CT/ATGGAAGGCTGCACTGGATGAGGTCAAAA
WI-3600b	146	G C	GGTTCTAACC TGGATATAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGAACCTCTGCTGTTTCCAGAGTGTGATTATCCATGCCCTG ATAGTTCTGT/ATGAGCCACCTAACTCGTTTCTGCTTAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACTGGATGAGGTCAAAA
WI-3600a	78	T G	CCATGCCCTG ATAGTTCTG	GGAACGAGTT TAGGTGGCTC	TAAATCATGCTTATTTTACAAAGTAATCCACTCACAATAGGCAATTGATGTCTCTTTCTGTAA GAAAAGCTCTCATGCTCTTCTGAACCTTCTACTTACTGTCTGTATGATGCACCT/CT/CTTTTGG ATAGATGGTTGATAGGAGATGGTTGTTAAGACACAATTTACCTTGTGTTTTCAGGCAGAAATAG ACTCTCTCTGTGTATCACTGAATGAGTTCCAAAAGCTTTATGCTTAC
WI-3678	125	G T	---	---	AAAGCGATGTTGAGATACCACATTCATGAAAAAGTAAAAACACACACAAAAATGACATAAAA T/AT/AAAAACTACTATAGTTTATGAAAAATGACTTCCAAATTCAGAGAAAAAGTCACCTTAAACAGG ATTCTCAATTCAATCCAGAACTACTCTCTGTCTTAACTTTGACTGCACAG
WI-3687	67	A C	---	---	TCATAAATGTGAACCAAGAAATCTGACACGACCTAACTGCCAGTCCCTCAGTTATGTATCAATGA AAAACT/CTACACCGGTTCAATGAAAAACAATGATGGTGAGCCCATGCCCCCTATTTAATGAAAAA GATCTTGGGCAATTAATCTC
WI-3735	72	T C	CCTCAGTTATG TATCAAAATGA AAAC	GGCTCACCAAT CATGTTTTT	

WI-1819	51	C T	---	---	GAAAAAGCAGGAAGCCAGGACAGGACAAACATTTTGAAGAGTCTTTAGCAAC[C/T]TTGCTGGATCCG AATTTTAGTGTGATTGGCAGGCAATGCGGGTAACATGTTCCAGTGTTTTAACTTGCACAGAAATTGC CAGATTAGCGATTGTTGACTTGTCCAATTAATGAATGTGGAAAAAAGGGTGGTAACCTGTT AAGCCTGCTGCAATGTTAGACACGAGGGTGGGGTGGGAGGTGAATACC
WI-3746	116	G A	---	---	GGCCTATTACATGACACTGGGCCAAGATCTTGCCTTCTTCTTCAATAGATAGACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGCTTCATCATCTCTGTCTCTGC[G/A]GCCCCAGGATAAAGCA GGCA
WI-3867	49	T C C A A	TAAGATAACC ATACTAGGTAC ATCCG	---	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTGACAA[T/C]CGGATGTACCTAGT ATGTTTATCTTATCTGACAGAACAGACACTGTGACACAGAGATTGTTACTTGAACAAAGACACAGT CATTAAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG CATC
WI-3898	25	A C G	TCGTCGGTGT CTCTCC	---	CAATGACCAATGTCTTTAGAAAGCAG[A/C]GGAGAGGACACCGACGAGACACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGACGCCACAAAGGTGAGGAAGCAAGGGTGTGCGCCACT GGACATTGTCCCTCAGAAAGTACATTCAAGCCCTGGACGGTGTCTTAACTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAACTCCGCTTCTCACCTGACAAAGTG[A/G]TATCATGTGCTACACTGC AGTGTTTATAATGCTGCAT
WI-3901	114	A G	---	---	CTGAGGAGATTGATGCTACTTTAACCCTGAGGAACCTTTTATACCTCCCTGAGTTTGTGCTTGCCTGCAA GACATTGCTGATTCTTCTCAAGACTCACAG[C/T]ACCATCCTTCTTCTGCTTAGACCTATAACTAG ACTCAAGTCCACAGAGGCGCTTAAAGTAAAGGTACAAAGTGTGACCCCATGGGAGGTATGTTACGCTA CAAAAGAG
WI-3914	99	C T G C	TCTAGAAGCAA TGAAGGATGG	---	CCACTCCCAGGCCAAGAGCGTCTCTATGAATCAT[G/A]CATTGTTCCTGTTATTGCTGTTCCACAGAGT GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC
WI-4019	33	G A A	AACAGCAATA ACAGGAACAA ATG	---	TAATTCACATTGCTCTGTTTGTGCAATTTATGCTTCTCTTATGTAACACAAATCACCAACATTGAGG TCTTAGTCATTGCATG[A/T]GTATAACAAATTTGTCACATTAATAGGAACCTCAAGCATAGTTATGTT ACATTTATTGCTAACAGCAG
WI-4091	84	A T G T C A T T G C A T G	TGAGTCCCTAT TAAGTGACAAT ATTGTT	---	TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCCCTTTTGGGTTAGGTGGCTTCTAAGATGGTAAT ATCTGTCCAAGTTTTTTTCTCTATAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT
WI-4160	117	A G C A C A G A A	AGCC	---	CGTTGCTGGTGAGAGTCAAAATTGATACAAACA[A/G]TCTGAAAATCTGTTGGCAATCTATTAAAGG AAATTGATAC
WI-4168	32	A G A A C A	ATTGCCAAACA GATTTTCAG	---	CAAATATATACCAGCAGTGGTGTAGCAATTTTCACTGCTGGGCATTACCTAACATAAATGAT

WI-4177	68 T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGGCAGCA ATCATGATG	ATGCCTGCGATATACCTTCCAAATGACTAGTATGAATAAGCACGTAATAAATTTACCTATTATATTT AT/C/CATCATGATTTGCTGCTTCTTCCAAATTTACTACAAATTTGATTGTACATGAGGCACATG ATCCCATTAACCCAAATAG
WI-4199	51 A C	CTCCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GCCATGAGCACAGAGGCTGAACCACTCCCCAAGTTAGTCAATATAAAAAA[A/C]CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAAAACAA
WI-5163	24 C T	CTGTCACTGGT CTGCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACTGGTCTGCTGTC[CTG]GGTCTGTTCTGCTGTTCTTCAATGTTCAACTGCTTGTAT CTGTGCCCCACTAAGGTATCAGGTTTATATGGGCACAGGATGAGGGCTTTGTAGACCAGAGTTTCTT GGAAATTGCAACATTTGGGCAT
WI-4250b	117 A G	---	---	TAAGTGCATTAACTGTACAAAGTCCACAAATACCTCTTCCACCAGTGTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACACAGGGGTGGGAAGGATCCTGTAAAGG[A/G]TAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4250a	94 G T	TCAATATGAG TCITGTGAAAC AGG	CTTTTACAGGA TCCITCCCAC	TAAGTGCATTAACTGTACAAAGTCCACAAATACCTCTTCCACCAGTGTAAAGCAGTTTAAATAACA GGTTCAATATGAGTCTTGTGAACAGG[G/T]GTGGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4255	68 G C	TGCTCCCCCAT CACCT	GGCCTACTTCA AGTTGTGTAAG G	TAAATGCTCTGGGAGATAATAGAAAGTCCCATCCCTCTGATACCTTGGTTGCTCCCCCATCACCT TG/C/CCTTACACAACTTGAAGTAGGCCCATCCAAACACTGTGTCAGAAAGATACTGTGCGAC
WI-4256	57 C T	---	---	ACAGCCTCTTCAATGGCACAAATCAAAAGCACCCAGTAAAGCAGAGGCAAAATCTGG[C/T]CTCAC CATTTGAAAAGTCTCTGAAGGATAAGGGAGTGAATGACTGCTAGAAGAGAATGATTGGCCTT
WI-4325b	71 C T	---	---	AGTTCACTGCTAGATGAGTAGACCATTGTTGCTTTTAAATGTACATGGGCAGGACCGGAAATGG GATG[C/T]TACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTCAAGATATCACCGCCAC CCAGGACACTGCCATATCT
WI-4325a	58 C T	---	---	AGTTCACTGCTAGATGAGTAGACCATTGTTGCTTTTAAATGTACATGGGCAGGAC[C/T]GGAAA TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTCAAGATATCACCGCCAC CCAGGACACTGCCATATCT
WI-4347	158 A G	---	---	TGGGCAGAAAGTCGGGTATGGCAAGTCAGGGTGGTTAACTTGGATGCCACTTCTGCTGTACCTTCT CTAGACTCTTGACCTGCAGGAGGATCCCTGGCCTCTGAGTTTATCATCTCCCACTCCAGCCAG GGCCTGTATCTGTTGAGGGCC[C/G]GAATCGTCACGGCTCACAACTGTGGAGGTAGGAATGACGA G
WI-1936	117 T C	---	---	CCAGTCTAGGCTGCAAGGACTTCAATTCTGGGGCAAGTCTGCTGTTGTAGGGTCAGAGGCAGCG ACCTGAGGGACACACAAACCAGTGGGACACCAAGGGTACTTGTATCACTTCTCTCCCGCAACCCCA AGCAGCACAGCTTGACGCTCCAGGAAAGACTCCTTACTTCCACTTGAGAAAAGGAGAGGGGAAGAGA AAAGAGGACTTTGACACACAACTTGA

WI-5204	54	C T	TAGATTTTATTGATGACAATAGGGAAGCCCTTTGTTAAATGGGTTTGAAGAA[C/T]GAAGAAAAA TGAAAAGGGAAGAAATTGACAGAAACCAAGAGAGTGTGAGGGGCAGCAAAATCCCAGTTTGACTGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70	A G C T C A A A A A	GGACCTTAAT ATTTAACAGA TTCCG	AGATAATTTTG TAAAGATAGTT TTCCG	AGATAATTTTG TAAAGATAGTT TTCCG	TTTCCCTTATTTATTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TAT[G/G]GCGAAAACATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCCT GTAGTCAAGGTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112	T G A T A T A A	TTGTATCAAA GAGATGGGT GATATAA	AATTAAGAA ATCTTTACATG GTTCTT	AATTAAGAA ATCTTTACATG GTTCTT	CCCTGAAATGTGCTTTGCTTCTCTCCCACTCTCTAGGAACTTTTCCATGTCAGGTGAAGGTTTTGA AGAGTCTTTAATTAACTTGTATCAAGAGAGATGGGTATATAAT[G/J]AAAGAACCATGTAAAGATTT CTTAATTAGTGAATTTTCATCAGGGCTCTTCCACTGCTATCAGTAAA
WI-4456	49	C T T A G T T C C	AGTTGAATTA TTCAGAAAAT TATAGTTCC	TTTCCTGTTAT GCATGAACCTTG	TTTCCTGTTAT GCATGAACCTTG	ACACATTTTCATTTGCTTTAAGTTGAATTTATTCAGAAAAATTATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACCAGGTTGGGCAATTGATTGAATTGT
WI-4461	49	A G C C T T C C	TCACCTGTTATT TTAAAATTAT G C C T T C C	TTTGACCTTTG ACCAATTTCA	TTTGACCTTTG ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAAATTATCCTTC[C/G]TGAAATTTGGTGAAA GGTCAAGAAATGAAATTCACATTTTAGATTTCTGGAAATTTTATTTGCGATGATAATGCAATGGGC
WI-4465b	75	G A	CTACTGGATTTTACTTTGCTCAAGCCAGACAACACAGTATATAAAGAAAAACAGTTAGTAATCTT TCACCTTT[G/A]TATTTCTCTCTACCTCAGGGAATC
WI-4465a	41	A G A C A C G A A A G T	AAGCCAGACA ACACGAAAGT	GGTGAAGATT ACTAACTGTTT TCTTT	GGTGAAGATT ACTAACTGTTT TCTTT	CTACTGGATTTTACTTTGCTCAAGCCAGACAACACGAAAGT[G/J]TATAAGAAAAACAGTTAGTAAT CTTTCACCTTTGATTTCTCTCTACCTCAGGGAATC
WI-1949b	160	T C T A A T C	GAGTGAATAA ATGAATGCCA	TGAGAGGTGGG GACAAAAA	TGAGAGGTGGG GACAAAAA	GGGGTTAGGACCTCGAGATCTTTTCAGAAAAGCAAAATTCAAAACCAATATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTTCAAGGCTGCTGACATGGCTGATGCTGAATATATGTTGAAGAAATAAA GGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCCACCTCTCACACCTTTTCCCTGG CACA
WI-1949a	86	T G A T G C T C T G A G T	CAGTGGTGAG	CCATGTCAGCA G C C T T G	CCATGTCAGCA G C C T T G	GGGGTTAGGACCTCGAGATCTTTTCAGAAAAGCAAAATTCAAAACCAATATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/J]CAAGGCTGCTGACATGGCTGATGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCCACCTCTCACACCTTTTCCCTGG CACA
WI-4529	64	T C A A G A T G	CCAAGTAAGT CTATCATTCTG	TTCTAAAAATA ACACTTCCTGA AAAA	TTCTAAAAATA ACACTTCCTGA AAAA	TGAGAGAGTTTTGGATTATTCATCCTCTGCAACACTCCAAGTAAGTCTATCATCTGAAGATG[T/C] GAGTCTCTCTTTATATCCTATGATTATTTTTCAGGAAGTGTTATTTTGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATGGGTGCTGGACAAGATGGGCCCTAGGATCATTTT

WI-4540	110 A	GCACATGTGG G C A T C C	GACAAATGCAGC C A T G C A	AGCTTTCCCTTTCTTAAAAATGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCCAGJTGATGGCTGCATTGTCCAGTC AAATGAGACAACCTTCCTAT
WI-4582	226 T C	---	---	AGCAAGCATCTGGCAAGCCTCGGTACCAAGAACATTAAATTCACCAACACACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGGCCAGTTTAACTTATTCTCTGTACACA AATACTTTATGGGAGACAGCATTTGTAATTCAAATCAATAAATGACTCGGTTTGGCTGTACAAGCAT AAACAGAAGCCTTGCAAAATATGGTTTCCTCCTTGTAGAAACCATTTGAT
WI-1965	105 G C	AG GCCATTGAGG AAGTGTITAA	GAATGGATGGG T C A T C T C T	CAAAGGTTAGTTTAACTTGGGGGCAACACAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCATTGAGGAAGTGTAAAGGCGJAGAGAGATGACCCATCCATTCCTGG GCTTCTTATATGACACCATACTATTCCACACAGATGTGGAGTCATTATTTGGTTGGTGTATGACAGT CATGG
WI-5248b	99 C T	TTG	AAA	TGTTTAAACCACATACAGTTTGTGCTGCTACGTTGTGTAGAGCAACCCAGAAAAATTAACGCCTAC CATTTTCACTGTTTTCTATTGACCGTACTTGCTGCTTTTCTTTTCTCTCTCTCTCTCTCTCTCTG CCCTCTTTTAACTAT
WI-5248a	38 G C	CTACGTTGTT	TGGGGTGTCT	TGTTTAAACCACATACAGTTTGTGCTGCTACGTTGTGTTAGCGAACCCAGAAAAATTAACAGGCC TACCATTTTCACTGTTTCTATTGACCGTACTTGCTGCTTTTCTCTCTCTCTCTCTCTCTCTCTG CCCTCTTTTAACTAT
WI-4596	69 T A	AGCACTGTGA	CCTAATAATG	CATTGGTGGTCCAACTTCTGGGTGACATTACTGTTGACTTTGTCTGAAGCAGAAAGCACTGTGA CTTACATATTAGGCCCATCTCTGCTGAAAGCCTGCCTACAGCAATTTGTAACATATGGCATTGGG ACATATCTCTGAGCCCATCACTATTGACAAGATTCTCTTTTAAACAA
WI-5252	119 A C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAAGTCTTGGGAAAGGATTTGTGATGATCATTG AATCTGTTTAAATACAGAAATTAATACTGAATACCTGTGTGAATCATTTGCTTTTACJTAGCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGCCCT
WI-4606	61 A G C T	GCAATGCTAG AAAATTATGC	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAATGATAACCGAGCTGTTGTTCAAGCAATGCTAGAAAAATATGCCTAAGJGJ CAAGTAGACAACCTTAAGCACCTAAGGCAGAAATGAAAGTTCTCTCTGTGCTAATAGTCCCTATTCA ATTACCATTTATCGGGTAATTAACACTGGAAGTAATGCCAGGCTAATTTAGATTATGATAAT TACAGCTCTTTGCTATGCT
WI-5257	77 C A	GAGGCATGAA GCAAGAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATGGGGGCAAAATTAAGCATATGAAAAATACCAAGTGTGGCAGAGGCATG AAGCAAGAGGGGJCTTTTCATCTGCCCTGGTGGGTTTTTCAGTAACCTGCAACATGTCTTTGCCTCC CGGATGAAAAGATACCCCTCTATGACTCAGCAATCCACTCCTAGGTATGCACCCCTAAACATGGGTG GCAAT
WI-4649	50 C T	TCCGAATG	AATCATC	TCACGTGTTAGAAATTTCTTCTCCTCAGTGAGACCATTCTTCCGAATGCTGATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTGCTACCTGAATTTGATTTTTTAA AAAATCCTCCCAATATTG

WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT GTCCTT	CTGAAGTGTTA AACTGGATTG G	AACTGTGTGGTATGTTGTTGTTATTTTCTGGAGAGTCAGTTACTCTCACTAGATCATAAAGGG GACTTGGGAACCAAGATATCTCAAGACATTTAATCCTAGAGACACAAGAAAGTATAAGTTGTCTC TTATATTGCTTTTGA/GCCAAATCCAGTTTAACACITTCAGTAAGTT
WI-4677	82	T	C	TCCAAAAGTG ATTAGGTGAA AAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTTGAACATACGTCGACATTTTGGAAAAATTTGCCAAAAGTGATTAGGTGAAAAAAT GAGTTGAAATAAATGTT/CJAAGTTGAATAATGACACTGTTGAAATGATGAATCTGCTTTCAATTCA CATGGAAGGAGACTAGAACACAGCAGGTTTATAGGGGAATACTCAT
WI-4698	135	C	G	---	---	ATGATGCTATCATGAGGAATTCGTAGAAAAATTTTCACTGGCAATTGATTCAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTGATGTCAGTGACATTTCTTTCTTTTGACGGAAGAAACTTCAAJ C/GTTGAGAAGGCTTAGATTATATCGCTGAAGCCCATTTCTG
WI-4722	88	G	A	TGCATATGG AACACCACAC	AATATGGAATC TGCATTCAGTT G	CTTCCCATTTGCCAGTTAGATGACTGCCTCTCCACCAGCCTAGAAAAAGATGGGAGATTTATTTTC TGCATATGGAACACCACAC/GA/JCAACTGAATGCAGATTCCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGATTGTCA TAAAGGTCAGTAAATCAGTTTGTGTTGAGATTTTCAAGAAACGTGAAATTTATGAGTAACCATGGG TCAACTATGATC/AJCCAAAACAGCAGTGTTGTCTAAAAAATATGATAGTTTCTCTCCTGTCCACC GCAATGAAAAAGGAGTT
WI-2028	176	T	C	TGTTACGTT CCTGCTCATC	GGTTGGAAACT CAAATTACCTA GAA	GACTACAGCGCACAGACAGGCAATGTGTGGCTTGACAGGTGTTGTGTTTGTGTTTAAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGCTCTTCAGTTTACTACAGACCTCATCTCCTGGTTCTCTTG CACCCAGTCCACTTCACCTGTTTACGTTCCCTGTCTCATC/T/CJTTCTAGGTAATTTGAGTTTCCAACC TGTGG
WI-2033	183	T	C	GGGTGCTAGA ACTAATCCCTC	CAGTGGTTCCA CGTTCTCC	ATGTGTATGAGCTCCACATTCGCAGATTCAACCACTATGGATAGAAAAATATAGTATTCOCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTTCCAAAGTTTATACAGGACCAGTGTGGAAATTT AGCATTTCTGGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA/T/CJGGAGAACGTGGAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTTCTGGTGAAGGACAAGAGTTGAAGCAAAAGGACAAGGAGATCAACTGGG TAGAATAACTCATCGATCCCAAGGCTCTTCCACCATCTCCACTTCTACTCTGAT/T/CJ AGGCAGACTTATATGAAAAAAGGGA
WI-2034	150	T	C	CCACAGTGCA CCAAGGAC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGCTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGCCAAGA CCTCCTTCTGCGGTTTCAGTGAAGAACGATGAACCTCTTCACTCTCTACAGAGCTGGACTTCACCA CAGTGCAACCAAGGAC/T/CJGGACCTGCACTATCTTTACCCCTTCCGACACACAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	C T	TGTCCTTAAA GTGTGAAGT ATTAATTAG	ATTCTCTTG AAAGAAACAT CA	TCAGGTGACAGAAAAAGTCACATTTCTCAATCACTCACTGCTGTTATGCTCTTGCAAGTGT ATCCAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAAAAGTGTCTTAAAGTGTGAAGTATTA ATTAGATTCTATTTTATGATA[C/T]TGATGTTTCTTCAAGAGGAATTTGTGAAGAGGATTCCCATTT TGCAATTCATTGGC
WI-4782	113	C T	GATGCAGAAG ATAACTAGAA AATGC	GAACCTCTCG GTTATTTTCT GTTC	TCATTGACTTTTAGAGTTCCTTCAGTCTTTATGCTTATTTTAGGAAAAAAGTGGCTAGGAGAA CACAATTCAGGTTCTCTCCAGATGCAGAGATAACTAGAAAAATGC[C/T]GAACAGAAAAATAACCA GAAGAGTTCATTATGGTTTTCAGAACGATTAC
WI-4788	65	A G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAAT AAAATTTTGGC ATAA	AGGAGAGTTTGGCTCTTCCGGACTCTTGGAAATCAGTGCATAGAATCATCTTGCTAAGTCC[AG T]GAAAAAAATATATGCCAAAATTTAAATTTATCCAAACTTTAAGTCGAGATTATAATTGATAATTT AAAAACTATATTGAGTCTTTCTAAAAGATGGCGTATCACTCTA
WI-5300	38	T C	TCCAGAGAC CACTTCATTG	CTACTCTTCT ATTCATAATC CAAAAA	CTTACTTCCAAAGTGTTCCTCCAGAGACCCTTCACTT[C/T]CTTTTGGATTATGAATAGAAAGAGT AGGTGTTATTATTCCTCTTTTACCAAGGTGAATAGGCTCAGAGACAAGGTAGATGATGAGCCCCA AGGTCAGTGCAGAGAGCCA
WI-4818b	121	G T	TGATAATGGG GOCCTGTT	CCCTCTTTTA TATGTATGCCA GA	TATAATGTTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAAACAATCTTATATA ATAATTTATCAAGAAGGAAAAATATACATATGGGGTGATAATGGGGCCCTGT[G/T]CTCTGGCATA CATATAAAGGAAAGGCTAA
WI-4818a	43	A G C	TGCCATAGAC TAGGTTATGTC	CATATGTATAT TTCTCTCTTG AATAAAT	TATAATGTTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCC[AG]CACATGAATAAACAATCTTAT ATAATAATTTATCAAGAAGGAAAAATATACATATGGGGTGATAATGGGGCCCTGTGCTCTGGCATA CATATAAAGGAAAGGCTAA
WI-5317	139	T C	TTCCATTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTCCATTTTGTGTTGATTTCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAAATAATGATGTTATATATATACAAATTTCAACTCAACAGGAATCCATTTCTGGTAGCAGGT ATA[T/C]GGACTCATTTCTCTTTGCACTATTTCTAGGTTATTTGCAGCCCCGAGATCTACCCAGG
WI-4888	56	G A	GCAAGATATA AAGATTAAAG AAAGATAACA	CAATTCCACTA CCTCATTTATT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAAATGCTTGATAACTGGAGTAGTGCCCTT
WI-5328	44	A G	---	---	AACATTTTTAACCATGCTACATTTACAACACTGAAAGACAG[G/A]AAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATACTGGAAAGAG
WI-4897	93	A G	---	---	GCCTTTTGGAGTTTAAAGTCTTTTGGAGTGTCTTTTTCCTCCCACTAGGTACTCTCGGCCCAAT CCCCAAAAGAAAAATAAGCGCTTGG[AG]GATAAACAACATCTTC
WI-5345	29	G A	---	---	CCCTGCTATAGGTCAGTTTAAAAATCC[G/A]CCTGCTATGGTTGCTTGTGAAGCCACATCCACT GAGGTATATTCTGCTGCATTTTCTATATCACTCAGCTTCAGATCCACTCCATCAACTTGCAG

WI-5370	143	T C A T A A A C A A A	A A T A A G A T G G T A C C T T A A C T A	C A A A G T T G G T A C A G A G A A T T T C A A A	T G C A T G T T A C T T C T T G G A A T C A T A A A G G G A T C T G A G A G C C T A C A G T A T A T G G C A A C A T T A A C C A A T C T T T T G A A A T T T A C C T G T A T C C C A T C A T G G T T C A T T T G C A A A A A A T A A G A T G G T A C C T T A A C T A A T A A A C A A T T C T T G A A A T T C T G T A C C A A C T T T G C T T T T C
WI-9711b	423	T A ---	---	---	G A T C C C T T C A T C C C T C T C C A G A G A G G A G A G A G A A C A C A A G A A A A C G C C T G G T G C A G A G C C C C A A T T C C T A C T T C A T G G A T G T G A A T G C C C A G G T G A G A G A C G G C T T G C T G T A G T G G G A A A G C A C T G G A C C T C A A C A G T T G G A A A T G T T G A G T A G T C G T A T C C T T G A A G C T G T G C A G C A G C T T C A G T T C T T G C C T G T G G A A A T A T T T C C C T G A T A C T C T T A A A A T T T G A A T G
WI-9711a	390	C A ---	---	---	G A T C C T T C A T C C C T C T C C A G A G A G A G A G A G A A C A C A A G A A A A C G C C T G G T G C A G A G C C C C A A T T C C T A C T T C A T G G A T G T G A A T G C C C A G G T G A G A G A C G G C T T G C T G A T G G G G A A A G C A C T G G A C C T C A A C A G T T G G A A A T G T T G A G T A G T T A G C T G T C G T A T C C T T G A A G C T G T G C A G C A G C T T C A G T T C T T C G C C T G T G G A A A T A T T T C C C T G A T A C T C T T A A A A T T T G A A T G
WI-9702c	345	G A ---	---	---	G G A G A A T T T C A G G T G A A T G G A C T G C T C C C G C T C T G A T T C A C T G C T A C T A G C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C T C T G T G C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T T C T C A G T T T A T T C T A A C T T T A A T G A T C T C T G A C T T T T A T A C T A G C T T T A A G A G G T T T C A T T C C A G T G C T A C A G C A T C T G A T A G
WI-9702b	344	C T ---	---	---	G G A G A A T T T C A G G T G A A T G G A C T G C T C C C G C T C C T G A T T C A C T G C T A C T A G C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C T C T G T G C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T T C T C A G T T T A T T C T A A C T T T A A T G A T C T C T G T G A T T A T A C T A G C T T T A A G A G G T T T C A T T C C A G T G T G C T A C A G C A T C T G A T A G
WI-9702a	179	C T ---	---	---	G G A G A A T T T C A G G T G A A T G G A C T G C T C C C G C T C C T G A T T C A C T G C T A C T A G C C T G A G G T T G C A G A C T G G T C T G A A G G T G A C A G G T G C C C T C T G T G C C T A T T C A G C A A T T C C C T A C T G G T A T G T A T C A G G A T A G A G G T G A A T C A A G C T G A T A T T T G C A A C T T C T C A G T T T A T T C T A A C T T T A A T G A T C T C T G T G A C T T T A T A C T A G C T T T A A G A G G T T T C A T T C C A G T G T G C T A C A G C A T C T G
TIGR- A003N21	49	C A ---	---	---	T A T A G T A T T A A C G A A G C C T A G A A G C A G G C T G T G G G T G G T A T T G G T C A A G C A T A T C T A G G T A T A T A A T A A C T T T G A A G C C A T A A C T T T A A C T G G A G T G G T T G A T T C T T T T T A A T T T A T T G G G A G G G T T G G A T T T A A C T T T T T A A T G T T G T T A A T A T T A A G T T T T T G T A A A A G G A A A A C C A T C T C T G
TIGR- A004V30	203	C T ---	---	---	T G A T T A C C T C T C A A T C T A T T T G T A G A A T G G C T A C T T C A T A G G C A G A G C A G C C A C T T T T G G C T A A T T T T A A C A T C C A A A G C T A A T A A A T A A T C A A G A A G A A A T A G A G A C A T T A A C A A A A T A A A T T A T G T C T A T T T G G G A A T A C C T A A T A T C A G A T A C T A A C A A G T A C A G T G A T A A G A A T A A A A A G A T A A T A A T C A C A C A T A C C T T C T A G G T T A G T A G A A A A G C T G, T C T C T A G G T T A G T A G A A A A G T T

TIGR- A004W22	232 C A ---	---	GGATAATCAGTACAATAATGGGGACCTTAAACTGCTGTGATGCAGGAGTGGAGGGCTGGGCAGTG CCGAGGCAGGGGAGGACAGTGGGACAGGGATGCTCAGTGGTGGAGCCACAGCCCTGGCTCTGGA TGGGCATGGGAATGACCAGGTTCCACATCATGCACAGGGGCTGTAGCTTGAGTCCAGACAG GCCTGCCACATTGGTGCTGCCCGCCGCTA/C/A/CTGGAGATGCTCTAAAA
TIGR- A005D24 b	138 C T ---	---	CATAGAAAGGAGCTTTGAGTATTGACAGTTTGAATAATCTTTGAGATAATTGATTTTCATATTC TGTGGCTTTCAACCTCCATTACCTCTTGTCATTCCAACATCTTTATAGAGAAATAAAACCCAAATTT CTC/TTTTCACCAATTTAGTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAACTCCTTCACTTTAATAATTAAGGAAACAAT
TIGR- A005D24 a	123 A G ---	---	CATAGAAAGGAGCTTTGAGTATTGACAGTTTGAATAATCTTTGAGATAATTGATTTTCATATTC TGTGGCTTTCAACCTCCATTACCTCTTGTCATTCCAACATCTTTATAGAGAAATAAAACCCAA TTTCTCTTCCACCAATTTAGTTGATTATCATCTGGATTTTCACTCAAGATGCAGCTCCTAAGATTATTG TTATGTTAAATTCATAAACTCCTTCACTTTAATAATTAAGGAAACAAT
U03735	74 C G ---	---	TGAGTCTGAGCACGAGTTCAGCCAGGGCCAGTGGGGGCTGGGCCAGTGCACCTTCCGGGGCC GCATCC/C/G/TTAGTTTCCACTGCTGTCAGTGGAGGCCATCTTCACTCTTTGAAGCGAGCAG TCAGCATCTTAGTAGTGGGTTCTGTTCTGTTGGATGACTTTGAGATTATCTTTGTTCTCTTGGG GTTGTTCAAAATGTTCTTTTAA
U39840b	42 T C ---	---	GGTTGTCTGGCATAGCCATGCTGGTAGAGAGAGAAAAAT/C/CAACAGCAAAACCAACCA CAAAACCAACCGTCAACAGCATAATAAAATCCAACTATTTTATTTTCACTTTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATTGTTATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTC
U39840	56 A C ---	---	GGTTGTCTGGCATAGCCATGCTGGTAGAGAGAGAAAAATCAACAGCAAAACCAACCA CAAAACCAACCGTCAACAGCATAATAAAATCCAACTATTTTATTTTCACTTTTTCATGCACAACC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATTGTTATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTC
WI-8997	41 G A OCCC	AGTGCTCA	GTGGCCATCGATCTGACCGTCCCTGCCACTTGTCTCCC[G/A]TGAGCACTGGGTACAAACATCCA AAAGTTCAACAACACACCAAGCACTGTGTCTCATGGT
WI-7008	180 A G ---	---	TATACCACTTCCATTTGATGATGGAATGCTGCTGTTTCATGACCAACTTTATGGCTAGATGGTCAGAA AGCACCAGTTTCATGATAGGAGTTCAGGTCAATATGGTCACTGATGACCCAGAGTCAACATTTCAG TTTCCACCAAGCCCAGTAACAGGCCAAGAGCTGTCTCTCAAAAG/G/G/AGAGTGTATTCTGCAGA AGATGGCAGGGCCTTGTCTCGAAAGCCTAGAGACCGGCACTGTGATTACCT
WI-9005	26 C T GGGAACTCT	CGAATTTGCTG AAA	GGTCCCACGAATTTGCTGGGAATCT/C/TTGTTTTTCTTAAAGACTTTTGGGACATGGTTTGACTCC CGAACATACCGACGGTCTCTGTTTTTCTGGTGG

WI-7593	46 G A ---	---	TTTTGTTGCTCTGGACACCCTGCTCCAGGATGAAGGAGAG/GAATGAGATCAGTTTGGACATTCCTCTGAAATATAAGAAATCAACAAGTTACAGTCACTGTTGGGACTTCTTCTCTCTCCAAAGTGCATCTTGGGGAAAGGCTCCAGTGTTATCTGGACCAGTTCCTTCATTTTCAGGTGGGACTCTTGATCCAGAGA/GGAGACAAAGCTCCTCAGTGAGCTGGTGATATATCCAAAGACAGAACCCCAAGTCTCCTGACTCCTGGCTTCTATGCCCTCTATCCTATCATAGATAACATCTCCACAGCCTCACATTCATTCACACTATTCTCTGAAAATATTCCCTGAGAGAGAACAGAGAGATTAGATAAGA
WI-6962	78 A G ---	---	GCAGAGAAGAGAACCATGCCAGGGGAGAGGCCACCGCATC/GGTGACCCAGCGGAGGAGCCAACTATCCCAAATATACCTGGGTGAAATATACCAAATTCCTGCATCTCCAGAGGAAATAAGAAATAAAGATGATGTTGCAACTCTTAAAAAA
WI-7059	43 C G GCATC	AAGGCACCCA GGTCA	AGCAGCCATCACATGATCTGTTTTTACCACCTCACTGAAAGACACCATTTAT/CCTACCCCAAGGCAGAAAGTAGAACTTACTATTCAATTAATGTTGACACAATGGAAATGTC
WI-9063	53 A C TT	CACTTCACTGA AAGACACCAT	AAGGGCATTGAGACTATAAGCGAGTAGACAAATCCACACATACCATCTGTAGAGTTGGAACGTGCATCTTTAAAGTTTTATGCATATATTTAGGGCTGCTAGACTTACTTCTCTATTTCTTTCCATTGCTTATCTTGAGCACAAATGATAATCAATTAATACATTTATACATCACTTTTGGACITTTTCCAAAGCCC
WI-7079	293 T G ---	---	TTTTACAGCTTGGCATTTTCTCGCCTAGGCCTGTGAGGTAAGTGGAT
WI-9074	38 A G AAAAG	GGTAAAAGTT CTTTTGTCT	TGGATGCCGAGGTAAAAGTTCTTTTGTCTAAAGAA/GAAGGAACTAGGTCAAAAATCTGTCCGTGACCTATCAGTTAATTTTAAAGGATGTTGCCACTGGCAATGTAACGTG
WI-7104b	249 C T ---	---	GGAGTTTGGCCCTTCTAAGGGAAGGAGATCTTTATCTTCTGTTGGCTTGACCAGTCACGTTGGGAAGAGAGAGAGTGGCAGGAGACCCCTGAGGGCAGCCGTTCTTCTTGGACTGAGAGAAGGGAGCC
WI-7104	157 C A ---	---	CCAGGCTGGAGCAGCATGAGGCCCAAGCAAGGGCTTGGTCTGAGGAAGCAGATGTTTCATGCTGTAGGCCCTTGACCCAGGTGGGGCCACAGCACCCAGCAGCATCTTTGCT
WI-7104	157 C A ---	---	GGAGTTTGGCCCTTCTAAGGGAAGGAGATCTTTATCTTCTGTTGGCTTGACCAGTCACGTTGGGAAGAGAGAGAGTGGCAGGAGACCCCTGAGGGCAGCCGTTCTTCTTGGACTGAGAGAAGGGAGCC
WI-8974	34 C T AAGAACTCA	CTGAGCCCTC GCTGGC	CCAGGCTGGAGCAGCATGAGGC/CAGCAAGAAAGGGCTTGGTCTGAGGAAGCAGATGTTTCATGCTGTAGGCCCTTGACCCAGGTGGGGCCACAGCACCCAGCAGCATCTTTGCT
WI-9161	61 C T CTTGGC	CCTAAGCATTG GGAA	CATACAAATGAGAGCCCTGAGCCCTCAAGAACTCA/CCTGACGCTCAGCCCTACACCAGTTTCCACC
WI-9014c	93 T C ---	---	TGGAGTTTCATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTTTAA
WI-9014c	93 T C ---	---	CTGTGAGGGTGACGTTAGCATTACCCCAACCTCATTTTAGTTGCCTAAGCATGCTGGC/CCTTCCTGTCTAGTCTCTCTGTAAGCCAAAGAAATGAACATTCCA
WI-9014c	93 T C ---	---	CCCTGTTCCCATGCTGACCTGTGTTTCCCTCCAGTCATCTTCTGTTCCAGAGAGGTGGGGCTGGATGTTCCCATCTCTGTCTCAACTTTAT/CCTGTCAGTGAAGTGAAGTCT

WI-9014b	44 C T ---	---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCTCCCAAGTCATCTTTC/TGTTCCAGAGAGGTGGGCTG GATGCTCCATCTGCTCAACTTATGTGCACTGAGCTGCAACTTCT
WI-7023b	206 C A ---	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAGACACCCCTGGTGCT CAGTGCCTTTTAAGTGCACTCCGCTGTGCTGACTTTGAGTGGATCAACATCTGTCTACGGGTCCCC TCTTTTGGCCCCAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAC A/C/A/CACACATCTTGTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C ---	---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAG/A/C/CCCTGGCT GCTCAGTGCCCTTTAAGTGCACTCCGCTGTGCTGACTTTGAGTGGATCAACATCTGTCTACGGGTC CCCTCTTTTGGCCCCAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAC CACACACACATCTTGTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T ---	---	---	CTGAAATCCCTCTCTGCCCTGGCTGGATCCGGGACCCCTTGCCTTCCCT/C/TTGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTGCCGACCTCTCTGGCCCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAGTTGTGAAGCAGAGAGAGAAAGCTGGAGAGGCCGTGGGCCAAT GGGAGAGCTCTTGTATTATTAATATTGTGGCGCTGTGTGTGTGTTA
WI-9171	62 G A ---	---	---	ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAATAAAGAAAGTAGAGATAATAATCA/G/A/ TTCTTACAACCGATGGTAATTAAGCTTGATTACAAGACTTCATGC
WI-9174	47 T C T	CTAGACCCC ATTCTCCTATT ACTG	TCTAGAGGTA TATAGACAGG ACTG	GTGTGAGACCATCATGGTGCCAGTCTAGGACCCCATCTCCTATTAT/C/CAGTCTGTCTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGAGCTATGGTCAAAITGAG
WI-7753	52 A G	CCATGTTCCGA GAAGAACA A	CAGAGGCTTG AAATACAGGG A	AAGGCCAGATGCACATCCCTGGAAGGACATCCATGTTCGAGAGAAACAGAT/A/G/ATCCCTGTATT TCAAGACCTCTGTGCATTTATTAAGACCTGCCCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTCTTAATCCATCCTGTAAAGTTAATGTGGGTAGAA
WI-9186	76 G A	CCACTTCTCCC CGCA	AAAGGGAAG TCTGACCTAGG T	AAAGAACTACAGAGGACGATGTCCAAACAAAAAATGGCATCACCTGTCAAAAAATGGAGTTCCACT TCTCCCGCA/G/A/ACCTAGGTACAGACTTCCCTTTCATCTT
WI-9193	94 G A CA	AGAATATTGT CTGCCTTAAAG	GGTGTGTGG TAGGGG	TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTGTAGCAATTGACAGAGATAA CTCAGAAATATTGCTGCTGCTTAAAGCA/G/ATACCCCTACCACACACACCCCTGTCTC
WI-9015	48 C T ---	---	---	TTTGATTGATATCGTGAAATCCTCAGCCGAGAAATGGGTGGATTG/C/TGCTTTGGTTAATACAT CTTCCCTAAAGAGATAAACACAAAAATCCATCCAGGTAGCTCGGCCACCAACTAAGAA
WI-7254	37 A G	GGTCTGAGAG AGGAGCCAC	GGAGTGGGTGT CATTAGGA	GGAGCCAGGAGACAGAGGCTGTGAGAGAGGCCAC/G/ATGCCCTAATGACACCCACTCCTAGCC CTGAGGCTCGTGCCTCAGACTGGGGAAGAGTCCAGGAAGGGGAGGAGCCAGCCACTCCTCAATGC TCAATGGTCCCCCTGAAATCAAGACAGG

WI-9231	32 G	CAGTCCCCA GATTGA	CACTGCCCCA ACTCAGAC	GTGACCCCTGTGAGGTCCGCCAGATTGA[C/G]CTCTGAGTGTGGCAAGTGTGTCAAAAGGGGCG TGCCCCCAGGAGATGAGGCTGAGAGCAGGGAGTTGAGCCGGAAGATCA
WI-7836	120 T C	CAAATAAACA ATGCAACGTTG	GCTCTCAGAAC CAAGATTAGA AATC	TTGTTTGGGAAATAGAGAGTTGAGATAAACACTCTCAITTCAGTAGTTACTGAAAGAAAACCTCTGCTA GAATGATAAATGTATGGTGGTCTATACTCCAAATAACAATGCAACGTTCC[C/G]GATTCTTAAT CTTGGTCTGAGAGCCATTGGTTTCAGTTGAGCAATCCCATACCCAGCT
WI-7286	65 T C A	CAGCTTCAGCT TAAGTGACAG	AAACAATCTA ACCAGAAAGCT TTAA	TCCATCCTTTTGGCCCTGCAGCATGTCTGCTCCAGAAITTCAGCTTAACCTGACAGAT[C/G] TGTTAAAGCTTTCTGGTAGATTGTTTTCACCTGGTGATCATGCTTTTCCATGTGTACCTGTAATATT TTTCCATCATATCTCAAAGTAAAGTCA
WI-7858	91 T G TAAAT	CTAAGCATGT ACGTGAATTTT	CCCAATTTTA TTAAAAGTTTA CATCTAT	CAAAATCTTGGAAATATCTCAAATGTTTAATAACAATATGAATTTTCTCATGCATACTATTACTACT AAGCATGTACGTGAATTTTAAATTTGTTATAGATGTAAACCTTTTAATAAAATTTGGGTGTGG GAAGATTAAGGGAGGGTGTCTCTGTGGTCTCCTCCCTGCCCTCTCCCA[C/A]GTTGGGAGAGACC TGATTTGCCAAGTCCCTGGACCTGGACCACTGAGTACTGGGCTTATGGTGGGTGGTAGGCAGG TGAGCGTAAGTGGGGAGGAAATGGGTAAGAAGTCTACTCCAAACCTAGGTCTCTATGTCTAGACCAG ACCTAGGTGCTCTCTAGGAGGAAACAGGGAGACCTGGGGTCTCTGTGGAT
WI-7860	50 C G	CGTACCTCCAA ACATAATTGA	GCTTGAGTGA AGTCTGCAGA	CAAGGCGTACCTCCAAACATAATTGATT[C/A]GTATCTCGAGACTTACACTCAAGCAATCCTGAGG AATCTGAGGAGGGCTGGCTACTGTCTCTGCACCTGTGCTGTTG
WI-9064	29 A G TTC			CACACTGTCTGTTCTTCAGTGTGAGGTCTGGCAGGGTCTGGGTAAGCCGGGTTCCACA GGGCCAGCCCTGGCAGGGGTCTGGCCCCCAGGTAGGGGAGAGCAGTCCCTCCCTCAG[G/T]AACT GGAGGAGGGGACTCCAGGAATGGGAAATGTGACACCACTCCCTGAAGCCAGCTTGCACTCCAGT TTGCACAGGGATTGTCTGTTGGGCTGAGGGCCCTGTCCCAACCCCGCCC
WI-7307	128 G T	GAATGTGAC TTCACITTTGGT	CAGGTAGAATT TTCGTGCCATT G	GAGGAAATGTGACTTTCACTTTGGTG[C/T]CAATGGACAGAAAATCTACCTGTGCTACATAGGAGAA GTTTGGAAATGCACCTTAATAGCTGGTTTACACCTTGATTTCGAGGTGGAAA
WI-9274	25 C T G			AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAAGTTCTTAAT TGTTTGCAGTCTTTTATGTTTATTATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACAGTTTTTTGTTTATGTTTAAAGTAACTTATTATCTCTGGATTTCATG AAGGTGAATATCGTTTTTGTAACTGAATAGAATTGTATAGCGATGA
WI-7313e	266 T C			AATTCCTTTCTGGTAATCAGGCACATGATGAACCTTTGATTAGTAGGTCTGTGATTAAAGTTCTTAAT TGTTTGCAGTCTTTTATGTTTATTATCATAGGTATAGGTGGACCTAAATTCCTTATCATATCTTTATT AATTCAGCCAGTGTATCCACAGTTTTTTGTTTATGTTTAAAGTAACTTATTATCTCTGGATTTCATG AAGGTGAATATCGTTTTTGTAACTGAATAGAATTGTATAGCGATGA
WI-7313c	256 C T			

WI-7424	131 T A	CAAGAGAGAG AGAGGAAAGA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGGAAGAGCAGAGATTAGAGAAAAAAGCCACCGGAGGAAAGG AAAAAACATCGGCCAACCTAGAAACGTTTTTCATTCGTCATCCAGAGAGAGAGGAGGAAAGAAAA T/AJACAACTTTCATTCCTTTCTTGACAGTTTCATAAACATTCACATA
X86400	118 A C	---	---	TCCTGCAAGAAAGTTCTCAAGCCTTTTTTGATTTTTGTGCAATAAGTACAGCTTTGCATAAGAGTGAAA TTGGCTAGCTTAATGGATCCATAAACTTCTCTCTAATTTTAAGTGAGAJ/CJCTCTTTAAACACCT GTTAAATTAATGTAGCAGTCTGAGAATCTAAAATATATGACCACCTGTTTATTGTTTCATTCATCCA TCCCTTTTCCCATGAATATTTCA
WI-8053	242 T A	---	---	GTGGCCACTACATGTTATAGAAACCATCATCTTGTCCACAGCAGTCTATGAATAAAAGGCTGAG TTATCACTAAGCAGGAGAAAGCAATTAAGAGTGCCCATTAAGAGGGACTTTTAAATCAACCTAA TAAACTCTAATTCGTCTGACTTTTAAAGATCTAAGGTCAATTTAATACATGCTGAAAGGGTCACA ATTAATCTTTTGATCTTTTACTCACTGTTAACTTATATAAT/AJITCAGAAC
WI-6190	165 G A	---	---	TACACAAATGAATTCGTTTTATTTCGGGTATGCATCCACATTCAGCAATTTAGTGGTCTGAACAGCAAG TGGAAGAGCGCAGCAATTTGCCAGGAGGTCAAGCCACCAATTTTCGGGATCTGCTGTGCACACCGG GTTCTCTTAATCCCTGCTGAGGATCTTG(G/A)GAAGCAGCAGCAGCACCACCAAGGCGATGCA CCGGATTCAAGGTTCTTTTGTTCCAGTTGTCAAGATTCACAACTAGACCCCA
WI-6275	148 G C	---	---	AACAGTCACCAACACATGACAACTCGCCAGGCAAGGCTTGCTTCCTCCCTCCTTTTGGTGCCC ATGTGCCTAGTCAGCAAGGTGGGGAGGACCGGATTTAGCTTCGCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAA(G/C)GGAAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAACTG ATTTGCTTTCAGTAACTGGTATGTCGAA
WI-6421	41 G T	---	---	ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTTTGTGTTG/GJGGGCTTCTGAAAGAAACCTTGC TGACAGCTTCTCACTGACCTGCAGGACGGAACCGTACCTGAGAGGGGATGGGGCTCTCTCAAAAA GAATATTTGGGGCAGAACCTGGAACCTGGCCACCAGGGACATCCCAATATCCCCCTCCTCAGGG CTCACCCGACATCCTCAGCCAAATGAAGGCTCTGAA
WI-6905	215 T A	---	---	GGGTGAGACGGGTTATTGTGCACATTTACACAGCTCACAGCGTCTGGGCTGGCAGCGGCCATGCTC CTGTGGTGGGCTGCTCTACAAGGGCGTTCACTTTCTTCACCACACTATGTACAGTCAGTGCTCCAA GGTGATGGGCTACAGTGTGCATCAGTGAGTCTGTACACACATTTTACATAAAATACACACGACTC ATACATGAAAAAT/AJAGAGCCTAAGGGCTGTATTTTAAATGAGAAAAA
WI-9420	202 G A	---	---	AACTGTTTACAAAAATAGGCTTTGCAAACTTCATTACTGAATGTAAAGTCAATGACTGTGTTGTTTT TAAAAATGTACCAAGGAAATACAAATTTGATAATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACGACAAAGGTGCAAGGTGCAAGGAAACCGGAACCCATTGTGTACACTGTCTTCACACAG TG(A)GCATTCCTTCACCTTAACTGCAGCTGTGCAAGATGCCTCAGTGIG

WI-9448	184	G A ---	---	TGGGGCTGCTTTTAGACTTCATTTCTAGAGCAGAGCACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCCTTGCCCATGGTGGTTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAAATGGCTTGTTGTTCCAAAGGCTGAGAGCTGGCACCAC(G/A)CACTGGTTTCTAAA TCTCTGGCTGGATTTATCCAAGGCGCATGTTCTTAACGTGCCCGTGAGCAG
WI-9470	204	G A ---	---	ATGCTAGAAAGAGACACAGACAAGGAGTTTTTCCCTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGGTTGATAATCAGATTCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCACGAATATGATCTCCCTAAAGCCCGAGATTCCTACTAGAGCCGCTGGGGACACTGATGAC AA(G/A)GCAATCAACTCATCTCCTCAAGCTACCAGGGCTCACCTTCCCAAG
WI-1245b	201	G T ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGTGGT TTATTAAATTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC(G/ T)CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGTGGT GGTTATTAAATTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A ---	---	TCAGTGATAAGGACAGGTCTAGAACAAAGGTTCCCAACCCCTGGCACCATGACAGTTTGACCCAAA TAACTCTTGTTCAGGGGACTGCTCTACACATTGTGGGATGTTTAGCAGCCTCCGTGGCTTCTACCCA CTAGATGCCAGCA(G/A)CACAAACACCCCTCCCAACAATCATGACAATGAAAATGTCCTTAGACATT GCCAAATATACCTTGTGGGACAAAATGGCCCTGATTGAGAACCACCTGGTT
WI-5385	110	G A ---	---	AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCCAATGGTGGGATTGGAAGAGG GAAGTCTCGATAATTTTAAACATATGGTTTCTTGCCAGGAATCG(G/A)CAATGCTAATCTATTGCTTAA TCTTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCTGAC CCCTGCTACGGGAAACATTGAATGCA
WI-5403	199	T G ---	---	ACCAAACCGTTGGCAAAGGCTCCCCAAGACTCACCACCCCAACTTGGTGCTTACCCTATGCCGGGTG GGATTGAAGAAATAACCATAAATATAATTGCTACAATTTTCCAGTAGTTACCAGGCACACGCCTAT TGGAAGAAATCATAAATGTAACCCCTACAATGTATTGCTCTCTGGCTTGGTCCAGGCATAGAGTT/G JGGCCTACAACCCATTTATCATTTGAACCCCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G A ---	---	TGATATTTTCCCTTCTAAATGTTATGATTAAATAGTGCTTTGTAGAAATTTGAAAAAATGTAAA TCAGAGAACAGAAAGAAATAAGATATAGTTGAAACCTCTAACAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA(G/A)JAGGGAATGAGAAAAAGCACACCAGAAAAAAGTGTGT GGCTTAAGGGGAAGCCCAAGGAAGTTAAGT

WI-5801a	48 A G ---	---	TGGTATTTTCCCTTTCTCTAAATGTTATGATTAAATAGTGTCTTTGTG[A/G]GAATTTGAAAAAATGT AAATCAGAGAACAGAAAAATAAGTATAGTTGAAACCTCTAACAAATTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGCCTGGGAAGAGGGAATGAGAAAAAGCACAACCCAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAAGGAAGTTAAGT
WI-5896	61 C A ---	---	TTCTATTTAAATCCTGTGCCCCATTGCAAGACTGCATTAGTCTGCATGAGCCTTAGTTTC[C/A]TAA AAGCCCCCTCACACCGAGGGACAATGTTCAAACTAAATGACTGCAGGTGAGCAATTCCTGTATTA TACAACTGGGACCAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAATAGATTATAAGGCTGTGGTGAGTTTATTTAACTT
WI-7461	153 C T ---	---	TATTACTAGGTTTCATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATCTAACGCTCCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTG TGGCAGGGACTGTGCTC[T/C]TGTTCCCTGTGGTCCCGGAACCCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCATGTGCTGCA
WI-9716	221 G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAACTCTGAGGCTTTAATGGTCCCTTGCTCTAAC GCTTTGGTACTTCTCTTTCTGAAGACCAACCCCTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCTGATGTTTCAGATGTGACTTCTACATTTCTGAAACTAGATGAGTTAGGCTCTCTCATCT CAATTGAAAATTCCTAGAA[G/A]AAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49 C T ---	---	TTTTCGTTAAGTCTTGTGAAGCCACACAGAGTGATCTACTCTCTTTAC[C/T]AAGTGTACTTTGCA TATATTTATGGGATGATCTATCCCTACTTAAGATTTCTCTCTCAGGTTAAATATCCATTTCCCT TTGTCAGGAGTTTCTATTGGCCCTTCTTCTAAACOCCTTAACCATTTCTGCTTATTCCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---	---	GAAAACTCGTTGGCTCAAGGAACTGTAG[C/A]AAATCTTTTTTTTATTTTGTGTTTTTAACTC AAAGAGTGGAGTTTGCATTGACCTTGTATGGCAGCTGCTCTTTTGTGTTGTTAAATCCTCTAGT GGGCACCTTTCAAAAGCAATTTAGAGCAAGGTGGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAG TAGCAAAATGGAAGAAAGGTTAATGGA
WI-10312	41 A G ---	---	AAGGCCAGTGGGAAAGCAGACAAAACACTCCAAGAATAC[A/G]AGATATAAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTGATGCTGATGAGGCGATGTCAGACAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGGTGAGTCTTGCCAGTCCCATAGTAGGTGTTCCATAAAATAAC AGTGACTAACTGAGGTAGAGTCACAGAAGAAATTTCA
WI-11152	179 C T ---	---	GATTTCTTGGGACATGCAGAGCAGATACGGCAAGGATCTTTGGGCATTTGGAAGGAAACGAGCCCTA ATTCATAGAAACAGACTCTACAAAGGACCAGTTAAAGGTCTCGCACCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAAGGGGACAAAGTGGGACAAAAGGCTTGTCA[C/T]CTGTCAAGAAACATTGAA AACAGCCAGTACATGCCACTGTATAGA

WI-1968	167	A G ---	---	TGGTGAGGAGCTGTAGGCTGAAAGAATAGTCTCTGCTCTGGTCTTTCGTTGGAAATGGATGAGTCCT TTTACAAAATTTTCTCTTGGCATGGGTGTTATGTTTGAATCATGGAGTTGGAAGACTTAGATTCA ATTTGGGGCTGTACAGTTTACTGGAAGTTGTTAGJTGAACTTGAACAAGTGTCTCTTAATGTCTCTCA GCTCAATGCCCTTCCCTGTAA
WI-4701	198	G A ---	---	GGGTTCAATTAACAGGCTTCCACTGGGTCTCAGATTGCACGGAGATGTAAAAATAGGAAGAGATAG AAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACACACATTAAACTCTCCCACTCTA CCGCGCAAGTCTACCTTTTGGTCTTTTATTTCTGCTAATGACCATACTATTCCCAATTAGA[G/A] CCATGTCATTTTTCAGAAAAGCAGTATA
WI-4823	164	C A ---	---	TTATCTTTCCAAACCATGTGTGTTTCTTCACATACCTTTACGTAATTTTAAATCATGTCAATTAATTA TGCACTTACTTGTGGTACCAGACATGCTTCCAAATTTGTAATTCCTTAACAACAGCAAGCATAACT GATGTGCCATCTTGTATTCTTAAAC[C/A]AAAGAAAAGTGTCTTTTGTGCATCTGCCCTCTCTGT CTTCTCTGTTTCACCTCTGTATTTCCCTATTTCAGCAATTCATGATTA
WI-4860	72	A G ---	---	AAAAAACAACCTTCAATTTGACATTTAAGAAGATAAAGAAAAACAACGATCCACTGTGTGTTGCTTT GATTTA[G]GGAGATAAAACCTGATCTCTAAGAAAATTAACCCAAAGCAGTACACTAAAAATAGCCT TTGTGTGTGTTTTCAGGAAAGAAAGCCAAATCCAACTAAGTTGCTAAGAAAATAATGTTTCATATCA CTCTAACTTCCACATAGACATTAAATATAGCA
WI-9705	111	C A ---	---	TGAAGGACCAGTTCGAATGCCTACCAAGGTAAAGTAAATCGGAGGGGAGGAGTAGGAGTTGCTT CCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCGGTGC[C/A]AAAAATGTTAACACTGATGC TGCTACAAACGCACATAGAAATCGGTGATGATTCGGTTCCTAGTAAGTAGCTAATGTTTAGATA TGATTGTTGAATTAATGTTGCTGTGTTCTTGGTG
TIGR- A004248	177	A G ---	---	CAATAATCTCTGCTTAGAAGTTGCTTAGGGCCATGGATTATGTAAGGGTGGGCAGGGTGGACTG AAGATCTGTTGGCAGGCTCACAGAGACGGGGTGGGGAGAGATCGTGGTTTCATGAGATCCCAT CTTGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGA[G]TCCCTCCAAATTTACAGGGCTCCC GTGGGATGGTGGAGCCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG
U17579	34	T G ---	---	GGGATTCAATGTGTCTGTCTCATCCCAATAAGCAC/TG/CATGACCTCAGCCCCCATCTCTTCTTCCG TATGTTCCAGAGACAGATAAGCTGGCCCTTCTCTCTAGGGGATCACAAATTTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTCTGGGATCAATTTCTATGGGAGCC TGGGAGAGGGGATCTTCTAGTTGA
WI-7747b	88	T G ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATA TATATAATTTTAAATTTGAT/GJAAAGCTGATTACTGTCAATAAACAGCTTCATGCTTTTGTAAAGTT ATTCTTGTGTTGTTGTTGGGTATCCTGCCAGTGTGTTTGTAAATAAGAGATTGGAGCACTCTGA GTTTACCATTGTAAAGTATATAATTTTTTATGTTTGTCTGA

WI-7747a	44	T C ---	---	GTGAGCGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGC[TC]TCGTTAACTGTGTATACATATATATTTTAAATTTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAAGTTATTCCTGTTTGTGTTGGGTATCTGCCAGTGTTGTTGTAATAGAGATTGGAGCACTCTGAGTTTACCATTGTATAAAGTATATAATTTTATGTTTGTCTCTGA
WI-7189	197	T C ---	---	TCCAGAAATTTCCCTCTCAGCTCATTTTGTCTCTCACAATTAAGGGAGTAGGTTAAGTGAAGGTCACATACCATATTTCCCTTCAACAATAATATTTTACAGAAGCAGGAGCAAAATATATGGCCTTTCTTCTAAGAGATATAATGTTCACTAAATGTGGTTATTTTATTAAGCCTACAACATTTTTC[TC]AGTTTGCAATAGAACTAATACTGGTGAAATTTACCTAAACCTTGGTTATT
WI-7850	57	G A ---	---	AGCCCCAGCTGGACTCATGGATGTGCACCCCTTGTCCCTGCTCTTCTGCCCTGGG[TC]ATCATGTA TCTGGCAGCTCTGTACCCCTCTGTGGTGCCATCTCTACCTCTGACACAGACTGCCCTGGCTTGAAGCTGAGAAAGCACAGGGCAAGGCAAGGACCACAGAGCCTCAGCCAGCCAGGATCCGTCCTCATTTTATTGGTGATGATGAATGGGAATGAAATCAGGGGGCTGTCTACTAGAGCC
WI-7907	69	G C ---	---	CTCTTCTTCATCCCATCACCCCTAAATAGGTCAGGTGAGGGAGGCTGGGAAGAGGTGGGAGGAGG GIG[TC]AGAAGTGAAGGAAGATAGGAAGGATATTACCTCTTCTGTTATTTTAAAGAAACATTGTTTGGTGACAGCAATCTCCCTGTCCCTATCACTGTAGAGGCCATAATTTATATCTATAAATATAATAAAAAGCAAGTCAAACTTGGATGATCAAGGTAAATTAATGTCAAAAGTTTAAAT
WI-7919	242	T C ---	---	GAAGGCAGCTGGATCACTCCCGAGTCCTTGGCAGCGCTTGTGTGGAACACGAGAGCTCCTCCTCAGGGCCCTGGCACTCACCTTCTATTCTGTATGTATTTGGTTAAACACTGTCAAAATAATAGAGATGTGCCAGATTTAGATTTCTTACCCTAATCTGTTTAAATATTGTAACTTTATCCATTTGAAAGTGTCAGCCCCATTACAGATAAGCTAATAATCTGGTCTTTAAGGAA[TC]JACAACTTT
WI-7928	101	T G ---	---	CTCCCTTCTGATGCTCTCAGCAGCACGTTGGGGCACACTTGTTCATCTTCTGACCGTTTGTGGGCTATCCCTCGAGTGCAGACATCGTCAAAATTCAT[TC]JACAAGAGGAAATTTTCATGCAGAAAGCTGTATGCAGGATGCTCACTGATGTTTGCACTTTAAACCTGAAATTCAACTCTTTATATAGGATTTTCTTTTCTATCTCCATCTCCTCATTAATAAATACGTACATTTTCGAGGTAATGGTA
WI-7936	131	T A ---	---	TTTTGAGTCAAAAGACTTAAAGGGCCCCAATGAATTAATATATACATACTGCATCTTGGTTATTTCTGAAAGGTAGCATTTCTGGAGTTAAATGACATATAGACATACACCCAAACACTTACACCAAACT[TC]A]ACTGAATGAAGAAAGTATTTGGTAACAGGCCATTTTGGTGGGAATCCAAAGATTGGTCTCCCATATGCAGAAATAGACAAAAAGTATATTAACAAAGTTTCAGAGTATATTGTTTGAA
WI-7944	99	T C ---	---	TACACGTTCCAGCCCGTGGCCCCACTCATCTGCGCGCTTGTCTTGGTTGGGGGCAGATTGGGTGG AATGCTTTCCATCTCCAGGAGACTTTTCATG[TC]JAGCCCCAAAGTACAGCCTGGACCAACCCCTGGGTG TGATGCTAGTAAGATTACCTGAGCTGCAGCTGAGCCTGAGCCCAATGGGACAGTTACACTTGACAGA CAAAGATGGTGAGATTGGCATGCCATTGAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---			TTTCTAGGCTGTACAGTCTGATGCATGATTTTTTATAAATATTTTCATACTCTTGTAATTTGGATCTTT TTTACTTTGAGCATATATTTAGAAATATGTGTAGTGTAAAGGATCTCCACAATGTCTGCAGTGTG AAGCAGGTTCAITGTGGAATAGTTTAAACAGTCAGGAAGGCTAAACTGGTCAGTATTAATGTGTAGC CCTACCAAAATAGCCAGTAGTATCTGAAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---			GGCCAGGAGATTAGCAACAAGGATTCACTGTACTTACTTCTGCCCCCTTTTATCTTCCCTCTTGCCCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACACTCAGTGTCTTGGCAGTGTCT [G/T]CTACTCCTCAGGTGCAGCATACATAACCCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAAATTGGCAAATGTCAATCAG
WI-140	252 C T ---			ATTTGAAGATTGGAGGGCTTTCAGAGGAAAAATAGATTTCAATTGGATCCCCCAAACTATAATGACA AGTTTTTAATAGGTGATCAAGGCTTCTAAAGTGAATGCAAGTTGTTACCAAGTAAAGTTTATA TCTCCATTAGCCAGCTCAITGGCAGAAAAATCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAAATTTAGTTTAAAAATGTGCTATTGTCTGATTGGCAATCTCTC/T
WI-198	218 C T ---			GAGGCTTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCGAGTCCCGGATCAAGTGTGGCACC CATGATGGAACCTCTTGCCATGGTTTAGTACCCTGACCAAGTAGTCAITCCATCCTGACTTTTAAAA TTCTAACACAGCCTTTGATGGGACAATCTCTGCTAAAGACTAACCACTCTCTTATCTTATCTTCAGCTA CCTGCTTCCCCTTTC/TGTTTTAACAAAGCATAGAAATATCTGAACAAT
WI-205c	146 T C ---			TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAAATAGCCCTCATCTCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTTGAGATGATGGGCTGACTTTTTCAT GCATGAGTTGTG/CJCCAAAGGCTTGATGGGAAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAACTGCATATGCCCTTTATTTTGTAGTCCC
WI-205b	146 T C ---			TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAAATAGCCCTCATCTCTAACTATGACTTGGTCGG AAGCCAAAGAACCTACTTCAACATTTGACCCATAACCTTCTTGAGATGATGGGCTGACTTTTTCAT GCATGAGTTGTG/CJCCAAAGGCTTGATGGGAAAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAAACTGCATATGCCCTTTATTTTGTAGTCCC
WI-234	165 G C ---			GAAGACTGAGTTCCAGGAGGTTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGCAACCCCAAGTNCCTTCCAGAGGCTCAGACTACCTCTCCATCTCCCCCT CTCCCCACAAACACAAATACAGAGATTG/CJAATTTCAGGAGCCAGTTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTGTCTTGTAGTTTCTCAAAATGGAAATGG
WI-276b	25 A G ---			AGCTTTTGAATCCAAAAACCACATJAGJCTTGACTCTCTTATCCTCTCTTGTGTAAACATCTATCC CTGAGGCAGAAAAATACAGAAACCCCTGTGGCTGCCTGAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCTGCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGTCTTATCTCTCTCTGCTGCTGATGACTGGGCAAA

WI-276	25 A ---	---	---	AGCTTTGAAATCCAAAAACACATAG/GCTTGACTCTCTTATCCTCCTCTGTTGTAACTCTATCC CTGAGGCAGAAATACAGAAACCCCTGTGGCTGCTGAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAAGCATCTCTCTGCCTGAAAGACCTCTCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGTCTTATCCTCTCTGCTATCCCTGATGACTGGGCAAA
WI-427	59 G A ---	---	---	TTTCCCAATCCACAGGTAAACTAATAATGGATGATAGAAATTTAGAACTACTTCCG/AJGTTT TTCCCTGGGAAATATTACAAACATTTGGGTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTCATCAGACAGGTAGAGGCTGACTCTGGCAGGATTAGTACCAGTGTGAGACTTTATGT ATTCAATTTATAGAGCCAGGCTTGTCTGTCAACCCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCGAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTTATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATACATAACTTCTCCACTTCC
WI-562b	106 T C ---	---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCGAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTTATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATACATAACTTCTCCACTTCC
WI-562	103 T C ---	---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGGTTACAGATTAGCCCGAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATTTTAAIT/CJAAATGGTCTTTTATTAATAAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATTTATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATACATAACTTCTCCACTTCC
WI-597c	141 A G ---	---	---	GTGTAATTTGGTGGCTTGCACCTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG/A/GJTAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATTAAC TTGATCTAATAATTCTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAIT
WI-597b	141 A G ---	---	---	GTGTAATTTGGTGGCTTGCACCTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATACATG/A/GJTAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATTAAC TTGATCTAATAATTCTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAIT
WI-597	136 A G ---	---	---	GTGTAATTTGGTGGCTTGCACCTTTCCACAGTAACCTTTAGAATNTNAAAGGTGGAAGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAAGTATCCTTAGGATATTCT GATTA/GJATGATGAATGACCCCTCCATGACTCTGGTACCTCATCATACCAATGTGAGAAATTATTAAC TTGATCTAATAATTCTCACAACTAATATACCTGAGAGAAATAAGTCTATTTAAIT

WI-611	66 GC ---	---	TTCAAATTTAACACCATTTGGGTATATTAAATTTNGCTCTATCCATAGTTCTAACCCCTCTTCTCT[G/ CJACAGTGAGACACCGCTTCTATTGCTTGCTTGACGTATTAACTGATTCGATCAGTCACCCATCTGGA ACCAAGGTTTCAATTTCTGCTGACCCCTCCCTCCTCACCTACTTGGCTCTGACTCTCTTCTTCTGGGCT GAACCTTCTCTGTGTGGCTGTCGGCTTCTCTGCTTGGCTCCAATAC
WI-681b	156 A G ---	---	TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTGAAGTATCTACCCCTTTA GGGATATTGTGAGAAATCAATAAGTTTACACAGGGGAAGCACTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATT[A/G]TTATACCTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCAAAATCTGTCAATGGTTT
WI-681	156 A G ---	---	TGAAGCCCTCTCTATACCCAAAGTGTCTTTATCTTAAATGCTGTGGTGAAGTATCTACCCCTTTA GGGATATTGTGAGAAATCAATAAGTTTACACAGGGGAAGCACTTTGNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATT[A/G]TTATACCTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCAAAATCTGTCAATGGTTT
WI-867b	119 G A ---	---	AATCTTAACAGCCCTTTTGATGCAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCAAGTATCTGGCACATCTTCCCTTTTCATCTCC[G/A]TTTGTGTGTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCCTCCCAAGCAAGCACACATTAGAACTTA
WI-867	113 A G ---	---	AATCTTAACAGCCCTTTTGATGCAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCAAGTATCTGGCACATCTTCCCTTTTCATCTCC[G/A]TTTGTGTGTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCCTCCCAAGCAAGCACACATTAGAACTTA
WI-867	119 G A ---	---	AATCTTAACAGCCCTTTTGATGCAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCAAGTATCTGGCACATCTTCCCTTTTCATCTCC[G/A]TTTGTGTGTTGGC CAAATAATATCTCCCCAGGGACGTCCTCTTTCTAATCCCTGAACCTGAGAAAATGTTATCTTATGC AGTGCTATGGTTGAATGTGTCCTCCCAAGCAAGCACACATTAGAACTTA
WI-871b	123 C G ---	---	TCATCAGACCTGAGATTTCAGCATGAAATCTACCAAAGGTACCAAAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGACACCCACCTACCTCATG[C/G]AACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTAAATGCACGTATTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGTTATTTGTACATAA
WI-871	123 C G ---	---	TCATCAGACCTGAGATTTCAGCATGAAATCTACCAAAGGTACCAAAATGTAACTTGTCCAAAACGA ATCTCAGTTTCTGCATATGTAATGGGAATGATAAGAGACACCCACCTACCTCATG[C/G]AACTGTT GAGAGAAATAATGAGACATTGTAAGTAAAGTTTGTAAATGCACGTATTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCCAATATGNCCTGTTATTTGTACATAA

WI-884	198 T C ---	---	AGGTTCTGGACTTGATGCTGGGAAACAATTGGGTNCTGGAGAAATTCCTATTTTGGAGTNTTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTTCCTGATCTATTGGGA ACTTCCTCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAGGAATA[T/C]G ATCCGCGATGCAACATTTATTCAGTGAACAACATGATGAAAATGAACATAAT
WI-921b	205 G A ---	---	CACITCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGACACTGCCAGGTGCACACAGGACAGTTATACTGG CAGTGATGCCTCTACGCCCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCCTCCGAG
WI-921	205 G A ---	---	CACITCCCAAGGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGACACTGCCAGGTGCACACAGGACAGTTATACTGG CAGTGATGCCTCTACGCCCTGGCCCCCAAGAAAGTCTTNGCCAGGAAAGACGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTCCTCCGAG
WI-945c	90 G C ---	---	GGCTGGGATGAGAGGTTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCTGAGTAATAAGAAA AATCATTAGATAAATGCTCATGACCAAAACAAAGTTCAACACANTAGGTGCAGCAGCANNNGGTT TTCTCTGGTCATAGAATCTCTTAAAGGGAATCATGACAGATTTTCTTGGCTTTA
WI-945b	90 G C ---	---	GGCTGGGATGAGAGGTTCTACTTGTGGTACTGGAGGTTTCACTGGCTTGTCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCTGAGTAATAAGAAA AATCATTAGATAAATGCTCATGACCAAAACAAAGTTCAACACANTAGGTGCAGCAGCANNNGGTT TTCTCTGGTCATAGAATCTCTTAAAGGGAATCATGACAGATTTTCTTGGCTTTA
WI-960b	167 C T ---	---	TTGCTTCAAAGAAAGTTCTTGTCTCAGGAAGTTATTCATTGACCAACCTAAAATTTTGTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAAATTTATCAAAGATGTTAAGTTATCTTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 G A ---	---	TTGCTTCAAAGAAAGTTCTTGTCTCAGGAAGTTATTCATTGACCAACCTAAAATTTTGTGAGTACAT ATCAAGCACAGGGTTCTGAGCAATGCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAAATTTATCAAAGATG/AJTTAAGTTATCTTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 T C ---	---	TCCACTGAGTATGGCTTTCAGTAGTTTATTATGATGTCCTAGGTACATTTGTTTATTGTTCTG CGAATGTGTTGATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTTCTGACCCCTTTCTGTGTTT CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCACTA[T/C]GCTGTTTACTCTCCTCTG ATTTTCTTCCATTATTTTATTGCTCTGGCTTCATTTTGTAAATNG

WI-1147b	204 G A ---	---	TTTGCCATTATTTGAAGATAACCCACACACCTTGGTGTCCAGGGTTTCACAGGTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCAGCCACCGCAACTTCTCCCTCTCCCTGCTGGCTC CTGAGCCAAAACAGGCAATTACCATAAATCACCTTGTAGGATGAACCTTATCTGGCCAAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAACACTCTCATCAGGCAGA
WI-1158b	147 C T ---	---	GCATTAGAGGGTTTCGTTAATGACATTCAGGCCCCTGTCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAATACAATGTGATGGTCTCCTGAGTGTCTGAATGCCCGCAGGTGGC TAAGTCTGGGG[C/T]CTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124 C G ---	---	GCATTAGAGGGTTTCGTTAATGACATTCAGGCCCCTGTCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAATACAATGTGATGGTCTCCTGAGTGTCTGAATG[C/G]GCCAGGT GGCTAAGTCTGGGGCTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124 T C ---	---	AAGTTACAGAAAAAATACCAGAAAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTNCACAGACACTTATCCCTAGACAGCCATTCTTTTGAATGN[T/C]GNCANT AAAAATGATTTGAAATGGGAATAAAGCCCTCCCTCTAATGATTTGACAGGTAGACCTTGCCCTAG GCG
WI-1305d	202 C T ---	---	TTCTCAATCCCAATCTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAA[T/C]TNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305c	46 C T ---	---	TTCTCAATCCCAATCTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTC ACATCCACTGCTTTCANTAA[T/C]TNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305b	153 T C ---	---	TTCTCAATCCCAATCTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAA[T/C]TNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATA TGCAGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA
WI-1305	202 C T ---	---	TTCTCAATCCCAATCTGTGTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAA[T/C]TNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNNATATG[C /T]AGGGCGANGTAATANGTATACAGNGANTCATACAGCCCTGCCTACCA

WI-1306b	248	A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAATCTTGTGNNNNNTNG GGCTGGGTGACTGTCCTGGTCAATTTAGAAGCCATAGAGATGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCTA/G/GC
WI-1306	240	A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAATCTTGTGNNNNNTNG GGCTGGGTGACTGTCCTGGTCAATTTAGAAGCCATAGAGATGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTA/GTCTTCCTAGC
WI-1307b	118	T C ---	---	GACAAGGCTGGTACTAGTTTCCAATTCCAAATCTATGTACACTTTCCTCAAGTGGACA GATTTCTGCATTATACCTGCTGGGTTGGGGAGCAGTGGTAGGCAAT/CJGTGAGATTGCTTT CCTACCCTCTAAATGTATCTTNCATAATTATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCCTTTGGTGTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTTT
WI-1307	118	T C ---	---	GACAAGGCTGGTACTAGTTTCCAATTCCAAATCTATGTACACTTTCCTCAAGTGGACA GATTTCTGCATTATACCTGCTGGGTTGGGGAGCAGTGGTAGGCAAT/CJGTGAGATTGCTTT CCTACCCTCTAAATGTATCTTNCATAATTATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCCTTTGGTGTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTTT
WI-1325b	169	T C ---	---	GAGAGATGCCAAGACAAGCAGAGGGAGAGAGCAACCCNTCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCCCTTGTCTCTC/CJACCCCTCAGAACCTCCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTAAAGTTAGGTT
WI-1325	165	C T ---	---	GAGAGATGCCAAGACAAGCAGAGGGAGAGAGCAACCCNTCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCCCTTGTCTC/CJTTCTTACCCTCAGAACTTCCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTAAAGTTAGGTT
WI-1327b	162	T C ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGCAGAAAGTCTGTATTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTAGTGCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTG/CJGAAGTTGGGTAGTACCAAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTTCCATCTCTAAG
WI-1327	175	C G ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGCAGAAAGTCTGTATTGTAAA ACACCAAGTGGGTTTAAATGGAATGCGTATGTGTAGTGCATATTCAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAGT/CJGTACAGGCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCTTACTGAAGAGGCAATGGTTCCATCTCTAAG

WI-1417c	31 C T ---	---	---	CAGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGCGGCAGATGTGAGCCCCACGGG GGTACAGCATGCTGCTGGCATTGGAGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCGACTTCGGAAGTTAAGGGCTCGCTTCAAAAAGCTGGTCCGGTTTGAGCGGTTGC AGCGAGGCCCTTAGTCCGATTTAATGTTGCTTTGTAGAAAAAGTCGC
WI-1417b	31 C T ---	---	---	CAGCCGGAAGAGATTACGTGGAGAGATGTC/TTTGGCCAGGGCGGCAGATGTGAGCCCCACGGG GGTACAGCATGCTGCTGGCATTGGAGGCCCCAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCGACTTCGGAAGTTAAGGGCTCGCTTCAAAAAGCTGGTCCGGTTTGAGCGGTTGC AGCGAGGCCCTTAGTCCGATTTAATGTTGCTTTGTAGAAAAAGTCGC
WI-1729	172 A ---	---	---	CCATGAGCAACAGCATGTTTCTACTCTGTGATGTGTAGGGGGCATGTATATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTCATTATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAGA TGTTGGAGAACTGAAAAGAGAGCTTACATGACCCCAATAGCAAACTCCACACATTTCCAGCA GATGTATGTCTCTCGTGGTNACCTCTCTCCACCATCACCTGTTTTT
WI-1732b	122 T C ---	---	---	TGCCTTACTCTTTGTTTCATCCCAACCATTTACATTTTGTAATTTGGAACCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAGGAGTNTCCCTGGGTCAACCCCTTT/C/ATTCAGTCT CTGCCACATGCTAGTAACGTGAGTGATGGTGTCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACTACTATTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1732	114 C T ---	---	---	TGCCTTACTCTTTGTTTCATCCCAACCATTTACATTTTGTAATTTGGAACCTCTAGGAGGTTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAGGAGTNTCCCTGGGT/C/TAACCCCTTTATTCAGTCT CTGCCACATGCTAGTAACGTGAGTGATGGTGTCATCAGTATAATCCTGAGCCTCCCAAGGTACAGC CTTTCACTACTATTCATCATATTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1750	97 A G ---	---	---	GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTTCCCAAAAAAGGTTTAAAACTGTGTGGA CATAATGTTTGAATTTGCAGTTTCACTTGG/AG/TTTAAGGTGTGCTGTTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAACCGGCTGCAGTCCCTGACTGAG CTACATTCACCTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---	---	---	GGTACACAAAGAAATGCTTCTGGAATCTAC/AG/TTAGCGCCCTAACATTTTGGCTGAGTATTAATC TGTACATGTGTAATGTGAACCAACCATGAAGCTGGGCAAGAACAAATCTAGGAAAAGTACAATTAC TGGAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTTCCCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAAGAAATATCATAAAAAAT
WI-1803c	77 A G ---	---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGTTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGAT/AG/AGTAGGGTAGAGCATCACACTTGGGAGGACATATTCTGGAGTNAGATATCCTG GGTGCTAATTTCAAAATATATCTACTAAAGCATGACTTCTAGAAAAATTAATTAATCTTGTCTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATAACTGGAATCA

WI-1803b	77 A G ---	---	---	CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATATTTTTCAGGCAGAA CCATTATGATAGAGTAGGGTAGAGCATCACACTTGGGAGGACATATCTGGAGTINAGATATCCTG GGTGCTAATTTCAAAATATCTACTAAAGCATGACTTCTAGAAAAATTACTTATTACTCTTGTCTCTCAA GGAAATGGGAATACCTATAATACAGTCTATTGAGGAAATAACTGGAATCA
WI-1837b	112 C T ---	---	---	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGCCGTTTATAC[C]/TGTCTGCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGGAACGTTTAGCTTCTGCTGGCT
WI-1837	112 C T ---	---	---	TTTACTTGGGATTTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAAATAGCCGTTTATAC[C]/TGTCTGCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAAAGACCTTGAGTGAATTTTGAGCT CGTGAACAACCTGGGAAGTCTGGGGAACGTTTAGCTTCTGCTGGCT
WI-1840b	79 G T ---	---	---	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCAATTAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACCT[G]/GAGAATCTGAATATTGAGCAGATACAAAGTGTGACAAACCTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAGTTCCCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1840	79 G T ---	---	---	TCACCTAGGGAGGTCGCTAAAAATGTAGCTTCAATTAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCACCT[G]/GAGAATCTGAATATTGAGCAGATACAAAGTGTGACAAACCTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAGTTCCCTAAAGAGCCATGAAGAATTATAAGACT ATCGCA
WI-1879b	110 C T ---	---	---	GGGCTCACTTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTTCTTTGAGGTNAAGGACCTGCCNTTTT[C]/TGTCTGCNAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGACCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T ---	---	---	GGGCTCACTTTTCATCAGAGCACATATCACGTGATAGTCTGTTTCTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTTCTTTGAGGTNAAGGACCTGCCNTTTT[C]/TGTCTGCNAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGACCTGTGCCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T ---	---	---	TGTTCTCTGGTCCAGGACCCGGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C]/TGTCTGAGAGGT AAAGTGCCTGCCCAACGGCGACAACTAGAGAGCAGCCAAACAGGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAAGTGCATGAGAAACCACTTTTCTTGTCTC

WI-1900	119 C T ---	---	---	TGTTCTGGTCCAGGCACCGGGCTAAGTCTTGCTGCATAATGGAATATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNNGCAATTAGCCCCATCTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTGCCCTGCCCAACGCGCACAACTAGAGAGGCAACAGGTGTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAAGTCCCATGAGAAACCACTTTCTTTGCTCC
WI-1943c	165 C T ---	---	---	ATTCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTACAGAGTCAAGC AGCAAGCCAAATGGGTAGGGAAGACCAAGCC[C/T]CTCTGAANCTGGTCCACAGTGGAGATAGTGAA TACAGGCAACCGNTGAGCATTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165 C T ---	---	---	ATTCAGTTTACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGGCTAANCATGCTACTTTACAGAGTCAAGC AGCAAGCCAAATGGGTAGGGAAGACCAAGCC[C/T]CTCTGAANCTGGTCCACAGTGGAGATAGTGAA TACAGGCAACCGNTGAGCATTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164 C T ---	---	---	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTTGGAGTGAGGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTCCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960c	270 A T ---	---	---	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTTGGAGTGAGGGATTCTGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTCCCATGCANGGTCNTCTGGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960b	270 A T ---	---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTTCTCATAGAGTNTGTTTTTAGTCTCGTAATAACTGTTGCCCTAGGAAGGTTGTT TTTCTACTGCGTCTGTGAAAGCCTTTCCCATCGAGTGATACAGTACTTTCCAGTTATGGAGATTIT /C/TAAACAATCAAACTGGCTGAGGCTGTTGG
WI-1977	203 T C ---	---	---	AAATCTAGAGCCAGAAAGTCAGCTCACGATTTATAAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATCTGCACAAAAC TAGCTAAAATC/T/CJTJTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAAAGCACTCAAAAGTTATGTAGAGTAGTGTCTCTGAGTCACTTTTTTCTACTCTCAT GGCTTCACCAATGCTTCCACTGGATC
WI-2012	102 T C ---	---	---	

WI-2013	127 C T ---	---	C T T T T A G A G T G T C A T T T C G G T T C C C T T C T G G A A G T G A T T C G T G T T A G A A A A A T A G A T G C A A C G T T G C T A A G T A C C T A A C A T T T A A C A G T C T C C A G C A G A T A A T G C T G A T A C T G A C A C T C T C A C A G A A A G A G A A T A C C C A T C A T G A G G A A G A G A A T G A C T T T T G T C A G T T A T G C T C C C G G T C C C T T C A C T G G A G G A T A T C T A G C T T T C T G A G C C C C T G G T T A C T G C A A T C C
WI-2032c	166 G A ---	---	A C C A G A C A T C C C A T C A G G A G T A G T C C T T C T G G C A A G C C A G C C C T G C C C T T C T G A T T C C C A A A A C C T C A A T T T T T C T T N A C T T A C T C A T A A T T G C T A G G A T A T C C A C A T A A C C A A A A G C C A A C C T A A C C A C A T C A C C C A A C T G T T T C T A G A T G T A C A C G A J T G T G G A C C T C T G T C T C A A C C T C C G A C T T T C A C A G A T C A T T G G T A G G C T C A C C T C C T G T A A T T G C T T C T G T T T T C A A A G G G
WI-2032b	219 C G ---	---	A C C A G A C A T C C C A T C A G G A G T A G T C C T T C T G G C A A G C C A G C C C T G C C C T T C T G A T T C C C A A A A C C T C A A T T T T T C T T N A C T T A C T C A T A A T T G C T A G G A T A T C C A C A T A A C C A A A A G C C A A C C T A A C C A C A T C A C C C A A C T G G T T T C T A G A T G T A C A C G T G T G G A C C T C T G T C T C A A C C T C C G A C T T T C A C A G A T C A T T G G T A G G C T C A C G C T C C T G T A A T T G C T T C T G T T T T C A A A G G G
WI-2032	219 C G ---	---	A C C A G A C A T C C C A T C A G G A G T A G T C C T T C T G G C A A G C C A G C C C T G C C C T T C T G A T T C C C A A A A C C T C A A T T T T T C T T N A C T T A C T C A T A A T T G C T A G G A T A T C C A C A T A A C C A A A A G C C A A C C T A A C C A C A T C A C C C A A C T G G T T T C T A G A T G T A C A C G T G T G G A C C T C T G T C T C A A C C T C C G A C T T T C A C A G A T C A T T G G T A G G C T C A C G C T C C T G T A A T T G C T T C T G T T T T C A A A G G G
WI-2054b	188 C T ---	---	C G T T T C T T C T A C A T C T T G G G N A C A T A A G A N G A A G A A G N A G C T G C T T T T G G G T A G T T T G C T C A G A G C T G C C T A G A G C N A G G A C A A G A C A G G T G A C C T T C A A A T A C C T T A C A G A C T T A G G A T T G G A T T T C A T G T G T G T G G C A G C C C A G G C T C A C A G A A C T A A T A C C T G C T G T C J T T C T G C C T C C A C C A G C C C T A C T C T A G G C T C A A G G A A T T T A C T G G A T G G G C T G C T T T
WI-2054	183 T C ---	---	C G T T T C T T C T A C A T C T T G G G N A C A T A A A G A N G A A A G A A G N A G C T G C T T T T G G G T A G T T T G C T C A G A G C T G C C T A G A G C N A G G A C A A G A C A G G T G A C C T T T C A A A T A C C T T A C A G A C T T A G G A T T G G A T T T C A T G T G T G T G G C A G C C C A G G C T C A C A G A A C T A A T A C C T G C T G C J T T C T C C T C T G C C T C C A C C A G C C C T A C T A G G C T C A A G G A A A T T T A C T G G A T G G G C T G C T T T
WI-2573d	129 T C ---	---	T G G G A T T A A A C C C T G T T T C T C C T C C C A G T T C A G T G C C T T A A T G T T G T G C T A G A A A T T A A C A T T A A C A G C A G T A A A A T A G C T C T T A A A T G C A C T T G C C G T T C A C A A G G T G T T C C G T G C T T T C A T T A T C A T C T G A T C T T C C C A C C A G G C T T A T T A T G C C T A G G T A A G G G T A A G C A A C A G A G G C T G T G T G A A G T G A A T G A T T T G C T T G C A C A A G G T C A T A T G G C T G G G C T T G G A C G A G
WI-2573c	165 A C ---	---	T G G G A T T A A A C C C T G T T T C T C C T C C C A G T T C A G T G C C T T A A T G T T G T G C T A G A A A T T A A C A T T A A C A G C A G T A A A A T A G C T C T T A A A T G C A C T T G C C G T T C A C A A G G T G T T C C G T G C T T T T G A T A T C A T C T G A T C T C C C A C C A G G C T T A T T J A G J T G C C T A G G T A A G G G G T A A G C A A A C A G A G G C T G T G T G A A G T G A A A T G A T T G C T T G C A C A A G G T C A T A T G G C T G G G C T T G G A C G A G

WI-2573d	129 T C ---				TGGGATTAAACCCCTGTTTCTTCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTT[C]TGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGTAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAGGTCAATATGGCTGGCTTGGACGAG
WI-2573c	165 A C ---				TGGGATTAAACCCCTGTTTCTTCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTT[T]GATAT CATCTGATCTTCCCAACAGGGCTTATTT[C]TGCCTAGTAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAGGTCAATATGGCTGGCTTGGACGAG
WI-2573b	165 A C ---				TGGGATTAAACCCCTGTTTCTTCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTT[C]TGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGTAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAGGTCAATATGGCTGGCTTGGACGAG
WI-2573a	129 T C ---				TGGGATTAAACCCCTGTTTCTTCCTCCAGTTCAGTGTGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACCTGCCGTTACAAGGTGTTCCGTGCTT[C]TGA TATCATCTGATCTTCCCAACAGGGCTTATTTATGCTAGTAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAGGTCAATATGGCTGGCTTGGACGAG
WI-2868b	60 A G ---				GACTTCATGCTCATGAACAAGCATTTTGCTTAATTTACAGACATTAAAGCAAGCTTTCC[A/G]CTC CCACTTCCCTCCCACTATCACTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGTCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAACGCTTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60 A G ---				GACTTCATGCTCATGAACAAGCATTTTGCTTAATTTACAGACATTAAAGCAAGCTTTCC[A/G]CTC CCACTTCCCTCCCACTATCACTCAACCTCTTCATCCACTTTAAAGAGGTTCTTTAGGTCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAACGCTTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131 T C ---				CATGCTGTGTAACCTCTGTGCTGCTGCTGCTCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGAT[C] AGAAATGAATAGAGCCCCATTTAAATTATATCACAGCTTTATGCTCCACTTCTGCTTCCCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT
WI-2870	131 T C ---				CATGCTGTGTAACCTCTGTGCTGCTGCTGCTCGGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGAT[C] AGAAATGAATAGAGCCCCATTTAAATTATATCACAGCTTTATGCTCCACTTCTGCTTCCCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT

WI-2954c	49 T A ---			TTAGCACATATCTGTGTGGGACTTAAGTACAGACAAAGGCATATAAAAAA[T/A]CAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954b	41 A G ---			TTAGCACACATATCTGTGTGGGACTTAAGTACAGACAAAGGC[A/G]TAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2954a	38 G T ---			TTAGCACATATCTGTGTGGGACTTAAGTACAGACAAAGGC[A/G]GCATAAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTGACAAATAAGTCCA GAG
WI-2971b	62 T C ---			ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTACCAGCATTTCTAAGAT[C/G] CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGTAACTCCTCTCTTCTTAATAAACCTAAC ATTTCTTTTGTCCCTGACATTCGAAAGGCCACGCTGGTGTAGATGATGCCAGATTGCAATCCT AGTTCTTTAATGTTATTCTGAAAGAAAACCTTTTACTTAGGGATTGTCT
WI-2971	62 T C ---			ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTACCAGCATTTCTAAGAT[C/G] CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGTAACTCCTCTCTTCTTAATAAACCTAAC ATTTCTTTTGTCCCTGACATTCGAAAGGCCACGCTGGTGTAGATGATGCCAGATTGCAATCCT AGTTCTTTAATGTTATTCTGAAAGAAAACCTTTTACTTAGGGATTGTCT
WI-2995d	133 A T ---			TTCTGGGAAAGAAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGAGCTGGANTTTTTTT[A /T]AATCTTTCTTTCTGGTGTAAAGAAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151 G C ---			TTCTGGGAAAGAAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGTGTAAAGAAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133 A T ---			TTCTGGGAAAGAAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAAGGAGGAGCTGGANTTTTTTT[A /T]AATCTTTCTTTCTGGTGTAAAGAAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

WI-2995c	151	G C ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTNATCAAGATAAAGACCTGGAGACCCGACGCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTCTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	A T ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTNATCAAGATAAAGACCTGGAGACCCGACGCAAAAGGAAGGAGCTGGANTTTTTTNA /TAAATCTTTCTTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995e	151	G C ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTNATCAAGATAAAGACCTGGAGACCCGACGCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTCTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151	G C ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTNATCAAGATAAAGACCTGGAGACCCGACGCAAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTCTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133	A T ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTNATCAAGATAAAGACCTGGAGACCCGACGCAAAAGGAAGGAGCTGGANTTTTTTNA /TAAATCTTTCTTCTGGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-3147	85	C T ---	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACGAC ATCTCACTTAGCTCCTTC/TCCCTGCCATATCCTGTTTCCCTTACTCTATCTCCTGAGACTTCTCCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTNNAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCAATACCTTGCAAGG
WI-3234b	68	T C ---	---	ATTCTGTAATGTTTTCACTGCTCCAGTAAATTCCTTATTGAGGTCCATGTCCATTACCTCTACTTA T/CJGACAAAGGAAGAACACACAGAAAGCCTCTGTTTGAATCTGGCTCTTATAAATACCTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATACATCCTTAAATAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTTATTTTATATCTTAT
WI-3234	68	T C ---	---	ATTCTGTAATGTTTTCACTGCTCCAGTAAATTCCTTATTGAGGTCCATGTCCATTACCTCTACTTA T/CJGACAAAGGAAGAACACACAGAAAGCCTCTGTTTGAATCTGGCTCTTATAAATACCTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATACATCCTTAAATAGCATATCAAAAATTTTAC TCAGTAATTCAGAAAGAAAGGACAATGGAATGTACTTATTTTATATCTTAT

WI-3292b	106	G A ---				<p>GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCTCCGTCOCAGCCTATGTTACTGTATGCTG/AJGGTATTGGATTGGGATGGATTACTT GCCATGAATAATTTCCATTGTTCTCATTAATGATTAATTAATTAAGTAAATATTATTNCCATGA GACACAATGGAAAAATGGAAAAACATTTCATGGAAAAAACCCATTTCATC</p>
WI-3292	106	G A ---				<p>GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACTCATCC TCCCTGTCCTCCGTCOCAGCCTATGTTACTGTATGCTG/AJGGTATTGGATTGGGATGGATTACTT GCCATGAATAATTTCCATTGTTCTCATTAATGATTAATTAATTAAGTAAATATTATTNCCATGA GACACAATGGAAAAATGGAAAAACATTTCATGGAAAAAACCCATTTCATC</p>
WI-3355	19	G C ---				<p>CCATGAACCATGGGCTACA[G/C]ATATCCTAACTTCAGAGTCCCTCTACTGGAGAGGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATACTATTCTTCCAAGCATTAAACATCATCAGAA AAAAAATCATCAAAAAAGTCGAAGTAGTTTINATTACCTTCACCTTTTCAATGGAAAACTTTATAA ACTGTGGATCAATTTATATTACTTTTGGATCAGTTTAGACTTTNAGTTG</p>
WI-3408	194	G A ---				<p>CCATGAAGAATGAGTTCCTCCCTCCCTGGGTACGCTAAGAATAGCACACCCCTTGAGAAATTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCCTCGCTCTAAGACACACCTTTATGCTTCNAAGCTTT CTGGAATTGGGATGAATCINACATTCAATGTGCACCTTCGTGTGGGATCACTTCTCC[G/A]TGCCCC ATCTCGNAGAAGCCACTGGGAAGTCGAAGGAGTCACTTCAAAATCAGG</p>
WI-3505b	131	G A ---				<p>TAACTTATGCCCTCATCTGGCTTACTGCTTAGTCCCATTTTGTATCATGAGTGCACCTTAAAAAATATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANNGGAAAAAATGTTGATGATACCT GTTTAATTGGGAAATATGTTGCATAT</p>
WI-3505	131	G A ---				<p>TAACTTATGCCCTCATCTGGCTTACTGCTTAGTCCCATTTTGTATCATGAGTGCACCTTAAAAAATATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACCTTCTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTATTCCTTATGGGAAAAATATATACAGCAAGAAAAAANANNGGAAAAAATGTTGATGATACCT GTTTAATTGGGAAATATGTTGCATAT</p>
WI-3564b	177	C T ---				<p>GCTAGTAAGGTTCCACCTAAATGGTCCCAAGTCAGGAGAGTCACTAAATGTTTTGAGAAATAAAAGT GAAATCAATGTGCTCCAGTGTATTCACATGGCAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCTGTCTGTTCTACAAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCTTCACAAAAACAA</p>
WI-3564	177	C T ---				<p>GCTAGTAAGGTTCCACCTAAATGGTCCCAAGTCAGGAGAGTCACTAAATGTTTTGAGAAATAAAAGT GAAATCAATGTGCTCCAGTGTATTCACATGGCAGTGCACAGAGGGCTTGAGCGTCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCTGTCTGTTCTACAAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCTTCACAAAAACAA</p>

WI-3649	64	A G ---	---	AATGTCATGCTGTGACTGACCTGTCTAACACCTTTCCTAGTATTCCTTTAGTGAAGATTCACAG[G] AGACCAAGTTTGCCTTACCTTACCTTAGTAGGCAATGATAGACTTTTAGTGCTACCAAGGGTACCTGC ACAGCCACATCATATGTCACAGTATGGTTGCAAGGACCTGTCTAGACTCTTTCTGCCTGCCTTGGTC TTCTGTTTACCATAATTAATGATGACATGCAACCTCAGAGCCCTTTTA
WI-3674b	133	G C ---	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCTCTCTAA ATTTAACTACCAAGGCGGAGTCTTTATAGTAATTAATAATGTTTATTTAGAAAAATAACAAAAT[G] /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAAATTGTAACCTGGTCAAATGATTGTT AATCTTAATTAAATTGTTGTTTATGTTTNNATTACTGCCAATCACAGCCAAG
WI-3674	133	G C ---	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCTCTCTAA ATTTAACTACCAAGGCGGAGTCTTTATAGTAATTAATAATGTTTATTTAGAAAAATAACAAAAT[G] /CJAAGAAAAAATGATAGTCAAGTTGTAGACACTATTTAAAAATTGTAACCTGGTCAAATGATTGTT AATCTTAATTAAATTGTTGTTTATGTTTNNATTACTGCCAATCACAGCCAAG
WI-3682	137	G A ---	---	CAATATAGACCAAAATGACTGCCACAAGAGAAATTAGTGGATCTACATTTAGAAAACCAATGTTTTT ATTGGCTCTCTCTCTCTCTCTCTTTTAAATGCTCTCTCCAACACCAATTCATTTATTCTTTTCAA TIG/AJAGCAATTTGTCCAAATTAAGTCAATGAAAAATAATGTACATTTTTCACAAAGTATACATTA GCCCTGCAAAAGTCTTATGCTAT
WI-3854b	194	G A ---	---	GGTATGTTGAGGTCAAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTGGCCCTTGA CAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACTAGGCTTCTTGATTAATAACTC TGGTTCAGGAAGGCAAGGCAGTTATGACCACCTTACAACTGAGGAATCAAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-3854	194	G A ---	---	GGTATGTTGAGGTCAAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTGGCCCTTGA CAAAGACCAAGGACAACTGTAGGACTTCTGCATGGTCTACCTCACTAGGCTTCTTGATTAATAACTC TGGTTCAGGAAGGCAAGGCAGTTATGACCACCTTACAACTGAGGAATCAAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGGTTATAACAGAGTCAGAGCCA
WI-4039	210	G A ---	---	AGCCAGCCACATCATGTTGAGTCTGCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT CCATTAAACAAGAACTCTTGATTAACATTTGATGTTTGGTGTACACTACAGATCCAAGATGACCTC CCCATCTCAAGGTCAACTAATTAAACACCTTAATCTATTTGCAATCTTTGTCATTACCATAACATATT CATGG[G/AT]CTGGGATAAGGGGTAGACATTTTATGGGAGGCATTA
WI-4110b	130	T C ---	---	GAAAAATGATGTTTGTATTTCCCTTCCCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT AACCCTTTATTTGATGAAACTCTGTCTATAATTAACCTTCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCT GTTTAGGTAAATAAAAGATGCCCAAGAAATTCAGTATTCAGTACAGTAAAAAGTAGCAACCATGGG GTAGGACAAAGTNCAGAAAAAGGGAGGAGGTTGGGGGTTTCTCTGGGAAGA

WI-4110	130	T C ---				GAAAATGATGTTTTGATTTCCCTTCCATCTCAGATTATTGGAGTGTCAATTAGAAAACCTGATAGT AACCTTTTATTGATGAAACTCTGTCTATAATTAAACCTTCTCTTCCTGCTTTATTTTGGCTTC/JACA GTTTAGGTAAATAAAGATGCCCAAGAAATTCAGTATTCAGTACAGTAAAGTAGCAACCATGGG GTAGGACAAGTNCAGAAAAGGAGGAGGNGGGGTTTTCTGGGAAGA
WI-4119b	168	G A ---				ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGACAGGACAAGACAGACAGAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTGTTTTTAAAGGGCTCTGTTGATCATCTTCA
WI-4119	168	G A ---				ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGGCTTGGGTGGGAAAAGTAATAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGACAGGACAAGACAGACAGAGAAGGGGT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTGTTTTTAAAGGGCTCTGTTGATCATCTTCA
WI-4123b	51	T G ---				CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAATAAGAAAGTG[T/G]TTAAACTATTT CAAATAACAATAAAGAAAACATGATGAAATTCCTCGTTACATAATTGTATAGAATTTAGTGGG TTCTCCATGACATTGGCTTGTCTTCTCAACAGTGGGTGTTGGATGTTTCTATGCTTTCTC AGGCACAAACACAGTGAAGAACCCTTTAGCAACATTTCTGCTGAATGTG
WI-4123	51	T G ---				CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAATAAGAAAGTG[T/G]TTAAACTATTT CAAATAACAATAAAGAAAACATGATGAAATTCCTCGTTACATAATTGTATAGAATTTAGTGGG TTCTCCATGACATTGGCTTGTCTTCTCAACAGTGGGTGTTGGATGTTTCTATGCTTTCTC AGGCACAAACACAGTGAAGAACCCTTTAGCAACATTTCTGCTGAATGTG
WI-4149b	145	G C ---				TTGTACATGTTTCATTCATCCCTCCCATCTTTCTGTCTTATAAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATCT GTGCTG[T/G]CCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGTAAGTGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4149a	137	T C ---				TTGTACATGTTTCATTCATCCCTCCCATCTTTCTGTCTTATAAAGAACCTCGCTTCTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTTTATTTCCATCAAAGCTTTCTCAGCATCTTCTATATCT T[C]GTGCTGTGCTTGTGAAGAAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGTAAGTGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4182	188	G A ---				TACACACTTTTCATTTGGTTTCTTATCTGAGTAAAGGACCATCCATTATTAACAATCCCTC AGTTCTATGCTTTAGAGTCTTATAGGACTACTGTAAATTTAGAGGGAATTAATCTCTTGGAGTA GGGGAATGAGTTAAATAATCTACCATGCCAATTCAGGGGACTGTGGTTAA[G/A]ATGCTCTCTCT TGCCCCCTTCCCAAGTCTTAAATCTTAG

WI-4230	93 T ---			AGAGACGTTGAATGGGGACATCTTTCTATTTCGATTTTAGTTTAAACATTTGATAAGAAATTTGATGAAA GTTTGTACACATCCAGATTTATCTTTATAGCAGAGAAAGTCTGGCAATAATAACAGACACACTGACT TTTCCATGGTAAAGAAAGTTAGAGAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTGAAT ACATTTTAAATGGAGGAGAAATGAATAGTGACCTTTGAAAATTTTGAATTTAIGG
WI-4241	118 C T ---			GAAAATCCATTTGAAGTTTGGACCTTGAACCTGATCTCATTAAATACCTTTTNCCTGTAGTGGTTGATTT CATTTTGAACAACAGACAGACGAAAATTTCCACTTAAATTTAAATCTCTC/TJAAGTATCTATGAT TTAGCACTGTTAGCACCAAGAACTGTGAAATTTATCTCCTAGATATCTTTCAGAACTCTAGGATGGAAG AA
WI-4271b	151 A ---			CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCCCTCCCTTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A ---			CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGGAGCCCCCAACCCCTCCCTTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 G A ---			AATCGAAACATTGATTTTGTAAAGGAACACATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATGATACCTTTTGA AGGTAAGATGTGAACCTATACA/G/ATNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACTGGAAGCGGTAA
WI-4389	156 G A ---			AATCGAAACATTGATTTTGTAAAGGAACACATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATGATACCTTTTGA AGGTAAGATGTGAACCTATACA/G/ATNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAACTGGAAGCGGTAA
WI-4488	31 A G ---			GATGACAAATTTGTGATTTGGCATTTTAAAG/G/GTACCAATCCATTTTCTGGCTTTCTGGTT TGTTGTTGAGAAAGTCAGGGGTAGTCGATTGCTCTCTTTCTAGTTCTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACATAAAATCAAATTTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 G C ---			ACCATCAATGATACACCTTCTAAATTTTATGATGATTAACTGGCTCTGTTAAAAATAAAAAACCT GTCCTGGACATTTGAAAATAAACATTAATTTGGTCAATTTCTGCTACTTACAAAGTACTGCACTA AACAAGTTAAG/G/C/GTTTGTGGAGGGGAAAAATCATAAAAATGCATAAAAAATTTCTACCACCTGTCA TTTCTGTCCCAATAAATAAAATTTTACATGCTT

WI-4584	144 A G ---	---	TTGGTTGGCATTAGCCTCATAACAACTATTTACAATCATAATTGTTACTCTTATTTACAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTTAGTCGAGAGCCAGATTTGAACCCAGGAATCCATT CACCGGTAC[A/G]TGCTACCTGGGTAAAAATGTTTAAATTAATCTATGGCATTAGATTTCAAAGA GTCTAATGTGGTTTGAATAAGGTGCTTAAATTTGTTTATCAGTATGC
WI-4639	185 C T ---	---	TTCTGCAATTTGAATGTATGGTCAGACTTCAGAGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAAATCCACCATTTAC TGACCATATGACTTGGGGAACATTATCTCACCTATCTGAGTCTGTATCC[C/T]CATCTTTAAATTGTA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAAATGAAATAA
WI-5327	63 A ---	---	AAATGAATCCGCTTTAGAGCAAAATACCAGTAAGGGCTGGTGCAGGATGGTGGCTGAGAGA[A/-]GATTACTCATAAAAGCATATTAAATTTTATAATATGGAATAATTAAGTAAATGTGAAT TGAGTTTGAAGGTTGCATGAGAGTAGGAGGAGGTAGTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAATGGCTCTTTCCGATGACAATGATGAACGTGTTCTAAGCAGACAG
WI-5390	87 C T ---	---	GCCTTTGAGAATGAAAAGGGGAGCCTGGACCATTCAGGGCTTCTTCATCTCTGATTATTTTGTGAT TTATTGTTCACTTATTAT[C/T]GTCTGTCTCCCTTCTGGTATGCTTGTGCATGAAACAATGAATTC CCCAGTGCCTGGCCGATTCTGGCTCTAGAGGTGTCAGAAAAAAGTTTCGGTGAATAGAAATTG ACGAATGGTTTCAGAAATTGAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87 G A ---	---	CCTTGCCTGCTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAGCAGT GCAACATTATTATTTAAATTT[G/A]AAAGAAACTTGTCTGAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGGTGAATCCACCCCATCTCTTTCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTCATAACAA
WI-5404	87 G A ---	---	CCTTGCCTGCTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTATTAGCAGT GCAACATTATTATTTAAATTT[G/A]AAAGAAACTTGTCTGAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTCCATGGTGGTGAATCCACCCCATCTCTTTCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTCATAACAA
WI-5545b	77 A C ---	---	TAGGAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATTCTTCCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTATTTTCATTICA
WI-5545	77 A/C ---	---	TAGGAAGGGGATGGTATGGCTCTGAGACATTTAAATCTATTCTTCCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCAAACACCTCTGTTTCTGACAGCCAAAGTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAAGANTC GAGATACACCATGAATTTATTTTCATTICA

WI-5860b	134	A G ---	---	ACTCAAGTTGGGGATAAATCAGAAGTTCTATGTACAACCTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAATTATGGATTGTTTACTCCCTAACCAACCTTCTAACTGAGGAACCTAC/A GJTATACGTGAATCATGTGAAGACATTTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-5860	134	A G ---	---	ACTCAAGTTGGGGATAAATCAGAAGTTCTATGTACAACCTAAATTTTGCTAAGATTTTATTGT TTCTTTTATATAAATTATGGATTGTTTACTCCCTAACCAACCTTCTAACTGAGGAACCTAC/A GJTATACGTGAATCATGTGAAGACATTTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCA ATTTCCAAATCATCAACTTCTGTAT
WI-6106	208	C G ---	---	GCAACAACCTATTATACCTGATCCAAACCCAGGTCTACTAACATTAATCAACCCTAACCAATAC TATATTGTCCTGTTCTGAATTTTCAATTAGAACTGATGAGATTTAGCATGGGATAAGTGCAG TGCAGAGATAGTAAACACTGCTCTTTTGTCCAGGAGTCTCAATGTGAAGTATAATCTTTACAGAG TAATT[C/G]ATAGTAGGTCAACCAAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129	T C ---	---	AAGATAGACAAACATATGCCAGACCACAAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C] AAACCTATATTNCTGTCCTGTGCATACCTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCTGAAATTTTATACCA
WI-6109c	147	T C ---	---	AAGATAGACAAACATATGCCAGACCACAAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCTAA ACCTATATTNCTGTCCTGTGCATACCTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT TGNAAAATTATCCCTGAAATTTTATACCA
WI-6109b	147	T C ---	---	AAGATAGACAAACATATGCCAGACCACAAACAAACACAGACCTGTCTATTTCTGAGAGAAATGTAC ATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAGGAAAAAACCT[C] AAACCTATATTNCTGTCCTGTGCATACCTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGT GNAAAATTATCCCTGAAATTTTATACCA
WI-6109a	129	T C ---	---	AATGCCTATCACCTTCCATCATGCTGCATAACTGATTGATTCATAATGCTTATTGTAGCACCTGTC TTCCAACACATGCTGTTTTGTTCAATGAT[C/G]GCATATCCCAAGTGCCCTAGACAATGCCTCCCATAC AGTGAACAGATTGTGACTAAACACATACCTTGTAAATCAATAAAATTAATCAACTTGGCATATGCAGG GAAC
WI-6112	96	T C ---	---	

WI-6244	103	T C ---	---	TAATTGCACAACCTTACATATCAGGGTTTCTGATTTGAAGGAAGAGAATATTCCTTTCTTTAGTGATT GCTTAATATTAAATTCATAATAAGTGCACCATCTCTT/CJGCTCCTTATAAATGTGTTTGAAGAAGG AAATTGAGTGTTGGGAATTAAGCAACCCAGGAGACATTTTATATACTCCTACAGTGGGGAAGACTT CCTATTTTCTTCCCAAGGATGGATACATTCTAC
WI-6268	124	C T ---	---	CTGGCCTTATAATCCAAAGTTTAGGATTAACTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTT GTCTACAAGATTCTCCTAGTAGGGCTTTGGGTGTTGGCACCCTTTGGCTCATT/CJTACTCTCCCT GGGTCTATTGACTTTCAGGGAGCCTAGAAGAGCTGGACAAAACCTGCTTCTTTGCAGAAAAGAGTCG GGGTTCCAAAGATTTCTGTTACGATTTTTTA
WI-6336b	234	C T ---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTCAAGGGCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAATGGACCATTGTG GTACCCCAAGTGCATTATGCTTGGTAGAGCC/CJTJGAGGACACTGACAGT
WI-6336	234	C T ---	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTCAAGGGCTGAGAGAGCTCACTCCCCC ATATATCCCCCTTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTCAGAGTAATAGATCACATGAATGGACCATTGTG GTACCCCAAGTGCATTATGCTTGGTAGAGCC/CJTJGAGGACACTGACAGT
WI-6381	92	C A ---	---	TTGGATACAAAAATTCAGTTACACAATCAGTAGCATTCAAAAATTAGTTATGAGTATTTATACAATTA CAAAAATGNTTCATGTTTTAACAA/CJA/GTATTTTAAAGCTCAAACATTTTAAACACAGGCACAAT ATTCTAANGGCATATGCATTCCACATGGGCTTTTGAATGTCCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGCAAAAGATCAGAGTTCCAG
WI-6436	198	C G ---	---	GGTTGAGGCATTGGGAAGGCAGAAATTGAGGCAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAGTCATGACAGACAGGAATACAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTGGTGTCATAATAAGAAGTTTAGACTTTGGGTGTTAGTAGTTGTAGTAGTAGGTAGCGTT/CJ GIATTGGGTGATTTCCACAGACAAGGTGATGTTCTAAGATTTGATATTATTG
WI-6449	186	C T ---	---	GAGGCCTCTTTGCTTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTTTGTCTGATTGGTGGTGCTCACACTGCCAGATTGTTAAATATTTTGAATAATC GTATCTGGTTCTATTTCATCTGCATCTCTGATCTTATGCTGGCTCTATT/CJATCCCTATTCTCTGA TCATTATGTCAGACCTGAAGTTCCCTCTAAATTTTCTGTGGTGATTATA
WI-6449	186	C T ---	---	GAGGCCTTTTGTCTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTTTGTCTGATTGGTGGTGCTCACACTGCCAGATTGTTAAATATTTTGAATAATC GTATCTGGTTCTATTTCATCTGCATCTCTGATCTTATGCTGGCTCTATT/CJATCCCTATTCTCTGA TCATTATGTCAGACCTGAAGTTCCCTCTAAATTTTCTGTGGTGATTATA

WI-6463	72	T C	---	---	GCTGGAGAGAAAAAGACCTCCAAAAGAGAAACTAAATCAGAGTCTCTTGAGCAAGGAAATTGAAA AGAACAT/CJTGAaaaaaaattAAAGTAGAACTCAAAGAGCCAAAAGTCCCAATTGTGTCCATTA TAAGAAATATTTTGAATGGAAATCTTAAGAATGATTTTATTGATCAGTTAAATGTTCTTCTCCTCCTC CAGTCCCATTTATATGACATTCGCGATGCTG
WI-6474b	76	C T	---	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAA/CJTGTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGACTAGAGGAGAACTATGTAAAGCAG AGGTATAGAGGAACTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76	C T	---	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANAC AGAGGCAA/CJTGTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAGGGGTGACTAGAGGAGAACTATGTAAAGCAG AGGTATAGAGGAACTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175	T A	---	---	GAACCTCAATTAACCTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCCGTGCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGATCAGAGT/AJGCTCCTTGTGAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175	T A	---	---	GAACCTCAATTAACCTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGAATGCCACGCTTCGAGGCCGTGCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGGAGATCAGAGT/AJGCTCCTTGTGAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149	G A	---	---	CACATTTGAATGCAACTGAGAAANTGGTTTTNTAGGCCTACCTTTTATTTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGGNTCCCAAGCCCA TTAGCAATATCTTA/GAJTCAAAATTTTAAAAAGAGAACAGGAAATAGGAAAGGCCTAACAGAGGAG TTAAATAAATGTGCAAAACTTATCAGTCTTC
WI-6564b	54	G A	---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGTCTGTGCTGAAATCTCAATTAATTTCTCCNCCTATCTCTTTCCAT GCTCTGCCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTTTTTGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTTAAATAAAGACCAACA
WI-6564	54	G A	---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCCACTGTTCCCTATGC[G/A]CACTGGCTTTG TAGGCATTCACATCATATGTCTGTGCTGAAATCTCAATTAATTTCTCCNCCTATCTCTTTCCAT GCTCTGCCTCATTTNCTCAGAAATGAAGGCATTTGATTATNATTTTTTTTGGTCTGTGTAAG GTTCTTGGCAGGAGAACATGCATATGACTTTTAAATAAAGACCAACA

WI-6608b	46 C ---			CTAATCACAGTAGCACTGAACATGGCTCTAGTGGTGGGCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTTCCTCTAGTCTCTCCCTAGAGCTAAATATGCACTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTCTTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCAGGCACCTAGCTACAAGGCCACACCAAGAAAGGAA AGC
WI-6608	46 C ---			CTAATCACAGTAGCACTGAACATGGCTCTAGTGGTGGGCTCAGT[C/- JAGTTCAGGCAGCTAAAGGGAGGGGATTTCCTCTAGTCTCTCCCTAGAGCTAAATATGCACTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTCTTAGAGGAAAAAGAACTGAACCTCCAGCACTAG GTAAACTGCAAAAAAGAAAAACACCTGTGCCAGGCACCTAGCTACAAGGCCACACCAAGAAAGGAA AGC
WI-6666	68 C A ---			GTTAGACAGTATCCAGCAAAAAAGGTTATTTTATACCTCTACTTTTCCAAACGAGGAAACCTCCCC AIC/AJAAATCCCATCAACACACAGCATGCTGGAAGGCATTCTGCTTACTCTGTGGTTTCATGTAA ATGTTGGGGTGAATCATTCCGCTCTCTTCTCAAGTTCAGGCTTCTTGGGTAGACCAAACTA ATACACAATGTTAGAGCACACAAGAGA
WI-6670b	120 A G ---			AGATTAAACATAATTACTGGGGCCATTGTAGGGTTNGGAGGAGTGTCTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCCTCTCAACAGTAAGCACACAATGAAC/AJTTGTTAGCCA GCATTGCCATTGAGGGCCGAGTCAAGGTTGTGGGCCAGAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAACTCTTAGAAGGGAT
WI-6670	120 A G ---			AGATTAAACATAATTACTGGGGCCATTGTAGGGTTNGGAGGAGTGTCTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCCTCTCAACAGTAAGCACACAATGAAC/AJTTGTTAGCCA GCATTGCCATTGAGGGCCGAGTCAAGGTTGTGGGCCAGAGTTAGACAATTTGGGGAATCTGA AAAAAAAAGAAATACAGAAATTGTAACACAGACACAGAACTCTTAGAAGGGAT
WI-6704c	33 T C ---			TTTGAAAAATAAATTCATGCACCAATGTTTAACT/CACACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAAGCTTACAAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGATCATGTCATTAATCGATTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T C ---			TTTGAAAAATAAATTCATGCACCAATGTTTAACT/CACACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAAGCTTACAAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGATCATGTCATTAATCGATTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T C ---			TTTGAAAAATAAATTCATGCACCAATGTTTAACT/CACACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAAGCTTACAAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTTAAATATGGTTGATCATGTCATTAATCGATTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106 G A ---	---	CCATGGACAGTTAAITTAGGAAGCTTCGACTTGTTAGATAACAGAGGAAGTCCCGAGTTATCTACCT ATTCCCTAAACACATTTTGTGAGGCTGGAATGATCCC[G]ATAGTAAACCTCAACATCCACACCT GCATAAACATCGCCTCCCAAGTGAATTTATTACTGAGTCGACACAGGATGTCACCAGTGAGCCTC ATCTCAGTCCATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148 G C ---	---	AAACAAATGGTGCATTGCATAATATTTGGTGCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G]C/AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAACTTACCCAAATCCCAAGTTCCCTCTTC
WI-6766	148 G C ---	---	AAACAAATGGTGCATTGCATAATATTTGGTGCACAGTATAAAACAATACAATTAGTTCATATAAC ATTGGATATGGACAAAATACACANGATCCTTTCTTTGTCTACGGAAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G]C/AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACAGTGGAGGNGAACTTACCCAAATCCCAAGTTCCCTCTTC
WI-6787b	97 A G ---	---	ACAGATAAAAGTCTTTATCCCTGTATGTTACATAAGAAAGTCTTTACAGACTTTTTTTTATACA ATACCTTGTGAGCAATGTTCAAATTCACAC/GJTTTTTACTGCATAAGATATCTTCATGTACAACCTGT ATGCTTTGCTCTCTTGGGAAGGACGCGTTAAAGACCTATGATAAACACACATCCACATGACAAAAGGA GAGTGCAATAGGGCAGAGTAGANTACTACAGGAAAAGAGTAAATTCAGGT
WI-6793	105 C G ---	---	GAACCCACAGGTCCTGTTATTTAAGGAGCATTTACATTAATGATAGCAAGTTTCAACACATTCOA TCAACAAGGCGGTCTTCAAATCAATCAGTCAACCC[C]G/GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTTGGCTGTAGGAAGTAGGTTAATGCCCTTAATCCCCGGAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCAGTTTCTCATCACAGGTAAAAGGCAAC
WI-6810b	37 T C ---	---	CACAATAATAAATCACTCCCTACCCTTGAAACCTTTA[T]C/JAGAAGCATTTTAAATTTACAACACA AAGCTCAACCGNACCTACAATAAGTCTAGTGTGTACGNGCCAGGGATAAGGCTGAACAATA AATTAACCCCTTAAATGCTATGNACAAGTACAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C ---	---	CACAATAATAAATCACTCCCTACCCTTGAAACCTTTA[T]C/JAGAAGCATTTTAAATTTACAACACA AAGCTCAACCGNACCTACAATAAGTCTAGTGTGTACGNGCCAGGGATAAGGCTGAACAATA AATTAACCCCTTAAATGCTATGNACAAGTACAATTTCTTTTGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C A ---	---	GCATGATTAAACCAGTGCAGAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACAATGAGCT GCAGGTAAC[C]A/TJGTGGATACCCCTGTGTCTACTNGCCCTCCAAAGGCATTGAGGGGATCATCA AAGATGTTGGACACCTTGTTCAAACTCTGGTTCAGGTGCGGCCTGTGCAG

WI-6817	145	C A	---			GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACTCATCACTAACTCAACAAATGAGCT GCAGGTAAC[C/A]TGTGGATACCCCTGTGCTCTACTNGCCTCCAAAGGCATTGAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAGGTGGGCTGTGCAG
WI-6819b	221	C	---			GATGGAAGCCATTTTATTTCTCTAAATTTAAATAGAGACITTTAATGGAAACATTTTAGTAC CATATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCTAGTAAAGGCC CGTCAGTAGTACACATTTCTCTATGGTCCCTCAACAGTTTTCATATACAAAATTTCTGCTATTTG CTTTAGCAACAGCAATAACTTTTGTGTTCCCTATATGACACCTAATATCCAG
WI-6819a	175	G T	---			GATGGAAGCCATTTTATTTCTCTAAATTTAAATAGAGACITTTAATGGAAACATTTTAGTAC CATATGTCACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCTAGTAAAGGCC CGTCAGTAGTACACATTTCTCTATGGTCCCTCAACAGTTT[G/T]CATATACAAAATTTCTGCTATT TTGCTTTAGCAACAGCAATAACTTTTGTGTTCCCTATATGACACCTAATAT
WI-6826b	154	A G	---			GCAAAAAGCTTTATTGGCTCCCAACAAATATCCCTTTTAAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTTGTACAT[A/G]GAGCTTAAATAATATCAAAATGCAATATAGATTGGGTGCACGTG TAAGCTGAATGCAAAATATGGCAACACACACTGGACTGGGTATACGTTG
WI-6826	154	A G	---			GCAAAAAGCTTTATTGGCTCCCAACAAATATCCCTTTTAAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTTGTACAT[A/G]GAGCTTAAATAATATCAAAATGCAATATAGATTGGGTGCACGTG TAAGCTGAATGCAAAATATGGCAACACACACTGGACTGGGTATACGTTG
WI-6857a	122	T C	---			AGTGCAAACTATTTTGAACAAAAGTAAACTATGAGTCACAGCATTTCAGCAAGACATCAGACACGGA AGAGTGAACAATATTTCACTAAGTAAATACAGCAGATGAGATGCTCTCACATGTA[T/C]ATTTAAT TATTCATGCTTTTCAATAGTCTCTAGTCAACTTTGAGTGTAAATTTCCACAAATATATAGCAGCTCA AACACAAATGCGAGGAGCAATGGCAAAAGTTTGGCAACTGTTTGGGCTAAT
WI-6865	153	G A	---			TTATAGAACTTATGGGGCATACNGTAAATGAACCTTCAACCTTAAATCTAAACAAACAGCTTG TTTGTTGCTGCTGCTGAAATCTCCCTGCTCACAAACAGCCAGCTACTNGGTTTCTAAAGACGTA ATTTTGAGGCAAACTTC[G/A]TAGAGCCATTCGTGCAGAAAGGGAAGGAGAGCTGTTTGT TTACCTGTAGTATGAAGATATCTTTGCGCTGTTAGAACTGAGCTCAATTA
WI-6909	73	C T	---			ATTGAAAACCTGGTTAGCAACAGATAAATACAAATAGAGCCTGGATATAAAAATGAGAGAAGATGC AGACTT[C/T]AAGCTTATAGAGAAAGTCAAAAGGAGCAAGTTTGAATCAGATTTTATGATAC GGAACAAAATTTCCCTTTTGGCAACAGGATTATTCGAATAATAAATCTGCCAGTGCCCAATCAG AAACACCATTTCCACAATATTTGCATGCCCTAGTTGCCTATTTTATACATATC

WI-6910b	163 G T ---	---	---	CACTCAAAACCTTTATTCATTGATTACAAACTGTACAATATTTACAAAGTTTAGGCATTAAATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAATAAATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/T]TGAGATGTAATGGAGAAATTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCCGGACCTTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144 A ---	---	---	GCTTGTTTTTTTGTGTTTTTAAGTGACACCTTGGCCCTGTGGGCATTTCTCACCTTATCTTACCC AAAAGTGCCCTTGGGCCAGCCACTGACTGATTTAAACCCAGAAATGTGGTTTTAAACAATGTGGT CGTGGTGAATTCAGGTGATTTTNAATTTCTATTTGGTAGTATTTTCAGATTTCCCCACAAAGAATG TATTGCTTTGTAAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175 T C ---	---	---	CAATCAAAAAGTTCCAAGTTTCAAGCTGGGATGAAAAGCCAGGCTTCTGACTTGCACCTGTGCAC ACTGGATTTNCCCTCTGATCCAGCTGCAGCCTCCCATAGAAAGTTCACTCTTAATTTTCATGCCCATG CTTTGTCTTGGTCCCTGTGAGGAAAGGGTCAAGGTC/AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175 T C ---	---	---	CAATCAAAAAGTTCCAAGTTTCAAGCTGGGATGAAAAGCCAGGCTTCTGACTTGCACCTGTGCAC ACTGGATTTNCCCTCTGATCCAGCTGCAGCCTCCCATAGAAAGTTCACTCTTAATTTTCATGCCCATG CTTTGTCTTGGTCCCTGTGAGGAAAGGGTCAAGGTC/AACTGTTCTATAAGGATGGGTAGG TATCCTGGCAAGATATTTCCCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79 G A ---	---	---	TTTTTATGAACATTTTCAGATTCCTCATATCAGCAGCATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAAATCCCAATCCTAGGTAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACATATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAATTTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6955	79 G A ---	---	---	TTTTTATGAACATTTTCAGATTCCTCATATCAGCAGCATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAAAATCCCAATCCTAGGTAAGATATCAAGTTACAAANTAC AAGTGCCGNTAATTAACATATAGGTAGTATATTAANCAAAAATGNGTTTTTNGCAATTTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6957	47 C G ---	---	---	AAACTAAAACCCCTTATTGCTCCAAAGTGTGGCAAAATAGAAAAT[C/G]TTTCAATTACATTAGG AAATCGGTGGATAACGGAGTATAGTTATCCACTTAAGAAGCATTCCAGTCAAAATATACAAAA ACAAATTCAGATTGCTTGGATCTGGTCATTTATGGCTGAAGAAGTGGATTTGAAAACCCACTTTAGG CTAAAATAATGTATATGAATAATGCATAGACTGTGATCTAGAAAATCATGC
WI-6996c	242 G T ---	---	---	ACTTCTAGTGCCTCTGTTACCAACCCCTCTAATGCCCTCTGGTCGCCGCACTTCTGTATGTCCTAGGCCCT TAAATCTGCCTGGGTCCCTCCCTCTGCTTTCAGCACCCAGAGGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGGAGGGGCTGCTGGACCCAAAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGCTGCTGACT CTCTCCTGATGGTGGGCCCTCTGTGCTCTTCTCTCC[G/T]GTCGGATC

WI-6996b	242	G T ---	---	---	ACTTCTAGTGCCTCTGTTACCAACACCTCTAATGCCCTCTGGTCGCCGACCTTCTGATGTCGGTAGGCCT TAAATCTGCCTGGCTGCCCTCCCTCTGCTTTCAGACACAGAGGAGGAGAGAGCGCGCAGTTCCTCTG CAGGAGAGAGAGGGGCTGCTGGACCCAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTGTCCTCTCTCTCCG/GTGGGATC
WI-6996	228	T G ---	---	---	ACTTCTAGTGCCTCTGTTACCAACACCTCTAATGCCCTCTGGTCGCCGACCTTCTGATGTCGGTAGGCCT TAAATCTGCCTGGCTGCCCTCCCTCTGCTTTCAGCACACAGGAGGAGGAGCGCGCAGTTCCTCTG CAGGAGAGAGAGGGGCTGCTGGACCCAGGCTCAGTCCCTCTGCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGGCCCTCTGTT/GTGGCTCTCTCTCCGGTCCGATC
WI-7021b	112	G A ---	---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCTCAAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTCCTGAAGCCACAGACAATATGGTCCCAAATG/AJCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAATCCAAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7021	108	A G ---	---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCTCAAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGCTCCTGAAGCCACAGACAATATGGTCCCAAATG/AJCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAATCCAAATTAATCAAACC ACTGTTATTACAGATAATAGCAACTTGGGAAATGCTTATGTTACAGGTTA
WI-7056c	118	C T ---	---	---	GGCAGTAGGACACACAGTGGGGTCTGCTGGGACCTTGGAGAGCCTGCATCCAGAGTCGGGTGG CCCTGCAGCCTCCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGAC/TGGTGGGAGCCTCT GGGCTGTTGAAGTCACCTTGTGTTCCTCAAGTTTCCAAACACAGAAAGTCATTCCTTCTTTTAA ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7056b	118	C T ---	---	---	GGCAGTAGGACACACAGTGGGGTCTGCTGGGACCTTGGAGAGCCTGCATCCAGAGTCGGGTGG CCCTGCAGCCTCCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGAC/TGGTGGGAGCCTCT GGGCTGTTGAAGTCACCTTGTGTTCCTCAAGTTTCCAAACACAGAAAGTCATTCCTTCTTTTAA ATGGTCTTAAGTTCAGCAGATGCCACATAAGGGGTTTGCCATTGATA
WI-7091b	153	A C ---	---	---	AATTCGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACAATGTTTATACCTGCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAATAGCATT/CJTCTTATCATTATCAGCCTTTTATGTATTTTCCAAAGTAAAAATATTA ACATATTATTCATTGGTCTCTCTTTTATCTGTTCTATATGAATGCTAT
WI-7091	153	A C ---	---	---	AATTCGCTGAAAAAGGAACCTACCTATCCTTACATTTACCTACTAATGTCTCTTAACATCTTAGAG GTCCATGGAGAAGGCATATGGAGAACAATGTTTATACCTGCTATAAATAGTATTCCAATCACTGTG CTTAATTTAAATAGCATT/CJTCTTATCATTATCAGCCTTTTATGTATTTTCCAAAGTAAAAATATTA ACATATTATTCATTGGTCTCTCTTTTATCTGTTCTATATGAATGCTAT

[illegible]

WI-7175	194 C T ---			CTCTAGACTAGTGCCTTTACCTTTATTAATGAACGTGTGACAGGAAGCCCAAGGAGTGTCTCTCACCA ATACTTCAGAGAAAGTCAGTTGGAGAAAATGAAGAAAAGGCTGGCTGAAAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATAATGGTTTACTGCTGTCATTGTCCATGCCTA(C/T)AGAT AATTTATTTTGATTTTGAATAAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273 G A ---			TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTGGCTTTTCTCTGAGCCCAAGCTGCCTGGAG AGGGTCTCGCTGCTACTGGCTGGCTCCTAGGGGAACAGACCAGTGACCCAGAAAAGCATATAACCA ATCCAGGGCTGGCTGCTGCACTAAGAGAAAATTCGCACTAAATGAATCTGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGA
WI-7178	273 G A ---			TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTGGCTTTTCTCTGAGCCCAAGCTGCCTGGAG AGGGTCTCGCTGCTACTGGCTGGCTCCTAGGGGAACAGACCAGTGACCCAGAAAAGCATATAACCA ATCCAGGGCTGGCTGCTGCACTAAGAGAAAATTCGCACTAAATGAATCTGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGA
WI-7182b	116 A C ---			GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCACTCTGAGCCTT/CJTCTCTCCTCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTTCAGCTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCTGGAAGCCTAGTACCCCAATT
WI-7182	106 C A ---			GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCACCAAAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCACTCTGAGCCTATCTCTCCTCTATTT TACTTGAGGCTGCCAATTACCAGCCCCACGTTTCAGCTCAAGAGATGCCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCTGGAAGCCTAGTACCCCAATT
WI-7191b	273 T A ---			ATAATTGCTTGTCTAGCCTGGCAAGATATTTTATAAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTTAGATAAATGCACAGCACCACAGCACCACATCTAAGCATTAGTGATGGTAGC TGATGTCAGCTTCATGTGGATTTAAGCACTCTAGAACAATGAAGCTTCTTGGCATAATTTAAGGAG CTCCCAAAATGIGTTACCTATTAAATTTGTAACCTCAGCAAGTAGAAGACCATTT
WI-7199c	112 T C ---			CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTTGAACCTATGAGCT/CJGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCATTCTTAATGTTTGTGTTTGTGGTGTCTGAATTTCTTTTATTAT AGTCTATAGTTTACTCTCAGTTCCTCACCATCATCATCTTGCTAA
WI-7199b	112 T C ---			CCCAGTGGTGAACAGAACCTCCCAAATTTGAGTTGCACCCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTCCTTGAACCTATGAGCT/CJGGGGCCTGACTAGGAAAAGT TGGGAGTTAAGGAGGAAATAGCATTCTTAATGTTTGTGTTTGTGGTGTCTGAATTTCTTTTATTAT AGTCTATAGTTTACTCTCAGTTCCTCACCATCATCATCTTGCTAA

WI-7216c	237	T C ---			TGACACTAACACTCTAATCAAGCGAATGTTGGAACACCACCATGACCTCCTCTGTGTGTCCTTTCTCCCC AAGGACAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCTCCAGAAAAATACGTATGT TTAAACCCCTTCTGCTATACATAGGAAAGACACACATCCACCTAAATTTGACTGTACTGTTTAA CTGTCAATTCCTGAGGCTAAACACAGTTTGTITTTTTCCTGTAAATCACCTT
WI-7216b	237	T C ---			TGACACTAACACTCTAATCAAGCGAATGTTGGAACACCACCATGACCTCCTCTGTGTGTCCTTTCTCCCC AAGGACAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCTCCAGAAAAATACGTATGT TTAAACCCCTTCTGCTATACATAGGAAAGACACACATCCACCTAAATTTGACTGTACTGTTTAA CTGTCAATTCCTGAGGCTAAACACAGTTTGTITTTTTCCTGTAAATCACCTT
WI-7220b	147	A T ---			AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTTATTTGTCCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAGGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAA/JTAAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATTTCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7220	140	A T ---			AGGATGATGCTCCAAAGGGGACCTTGAACCTATTCACCATTTATTTGTCCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAGGTAGTACAGCTTCAGTAATCAATGGGCA GTGGC/JTCTAGAAAAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGGTAACAAACCCCTATAAATTTCTGGCTTACTGCACATATTTAGTGTGTTT
WI-7226	232	C ---			GATCGAATTTTTCAGATGATTCGGAAATTTTCATTCAGGTATTTGTAATAGTGACATATATATGTATA TACATACACCTCCTATTCCTTAATTTTGTAAATGTTAACTGGCAGTAAAGTCTTTTGTATCATT CCCTTTCCATATAGGAAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTGTCAGTGAAAAATAA TTACCCACAATGCCACCAGTAACCTAACGATTCCTTCACTTCTTGGGTTT
WI-7228b	254	G A ---			ATAGCTTCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTTGGCTCCCAATTCATAA TATGTTCAACAGGAGATTACAAATTTTGTCTCTTGTCTTGTATCTATTTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGATCAGAAGATATCTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTAAAATAAGAATGTTATCCAACTATTAAGATATCTCAATGTI
WI-7228a	163	G A ---			ATAGCTTCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTTGGCTCCCAATTCATAA TATGTTCAACAGGAGATTACAAATTTTGTCTCTTGTCTTGTATCTATTTAGTTGATTTTAAATTA CTTTCTGAATAACGGAAGGATCAGAAG/JATATCTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTAAAATAAGAATGTTATCCAACTATTAAGATATCTCAAA
WI-7233c	213	C T ---			CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCGGTCTTGTGTACATCCATTTTCAATTTGTACA GATGTGAACCTTATTCCTTGTCACTAATTAATTTAAATTTATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTCTACTTCTTCTTGTGCCACCTTTTGTGGCAATATTAAAGTGAAGTGTCTAATA GTGTAAAGTAC/JTGTGCACAAAAACCACTGCCAGATAACCCAGAGGGGCTGTG

WI-7233b	213	C T ---	---	CGATCGTACTGCCAGTAGCATGTCTGTCTGTCGCGGTCTGTTGTACATTCATTTCAATTGTTAGA GATGTGAACCTTTATTCCTTGTCACTAAATATATTTAAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTTACTTCTCTTGGCACCTTTTGTGGCAATATTAAGTGAACGTGCTTAATA GTGTAAGTATCTGTGCACAAAACCACTGCCAGATAACCCAGAGGGGCGCTG
WI-7233	211	T C ---	---	CGATCGTACTGCCAGTAGCATGTCTGTCTGTCGCGGTCTGTTGTACATTCATTTCAATTGTTAGA GATGTGAACCTTTATTCCTTGTCACTAAATATATTTAAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGGTTGAGCCCTTACTTCTCTTGGCACCTTTTGTGGCAATATTAAGTGAACGTGCTTAATA GTGTAAGTATCTGTGCACAAAACCACTGCCAGATAACCCAGAGGGGCGCTG
WI-7238	128	T C ---	---	CGCTCTACAGACAGCTCACCATTTTGTCTGTATCTGTAAACACATTTTGTCTTAGTCTTTTCTTCTG TAAATTTGATGTTCTTTAAATCGTTAATGTATAACAGGCTTATGTTTCAGTTTGTCTTCTGTTT[C]CCTGTT CTGTTTTAAACAGAAAATAAAGGAGTGAAGCTCTTTCTCATTTTCAAAAGTTGCTACCAGTGTAT GCAGTAATTAGAACAAAAGAAACATTACAGTAGAACATTTTATTGCCTA
WI-7252f	520	T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTTCCACTCGCAGACGACGCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGGCCCTGGGCTGGAGGCTGCCCGGCCCTGGTCTCTGTTCTGTTCTCG GACACTCTAGAGAACGCGAGCCCTAGAGCCCTGCCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCTCTCTCTCA
WI-7252e	552	T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTTCCACTCGCAGACGACGCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGGCCCTGGGCTGGAGGCTGCCCGGCCCTGGTCTCTGTTCTGTTCTCG GACACTCTAGAGAACGCGAGCCCTAGAGCCCTGCCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCTCTCTCTCA
WI-7252d	540	T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTTCCACTCGCAGACGACGCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGGCCCTGGGCTGGAGGCTGCCCGGCCCTGGTCTCTGTTCTGTTCTCG GACACTCTAGAGAACGCGAGCCCTAGAGCCCTGCCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCTCTCTCTCA
WI-7252c	552	T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTTCCACTCGCAGACGACGCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGGCCCTGGGCTGGAGGCTGCCCGGCCCTGGTCTCTGTTCTGTTCTCG GACACTCTAGAGAACGCGAGCCCTAGAGCCCTGCCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCTCTCTCTCA
WI-7252b	540	T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCCGCCCTTCCACTCGCAGACGACGCCGGGACAGAG GCCTGCCGGGGCGCCAGCCCGGCCCTGGGCTGGAGGCTGCCCGGCCCTGGTCTCTGTTCTGTTCTCG GACACTCTAGAGAACGCGAGCCCTAGAGCCCTGCCCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCTCTCTCTCA

WI-7252a	520 T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCGCCCCCTCCACTCGCAGCAGCGCCGGGGACAGAG GCTGCCCGGGCGCGCAGCCCGCCGCTGGGCTCGGAGCTGCCCGGCCCGCCCTCTGGTCG GACTCTCTAGAGAACGCGCCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCGAGGTGGAACCTCAGTCATTAGACTCCTCCTCCA
WI-7265m	252 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTTATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCTTT
WI-7265l	231 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTTATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265k	121 T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265j	174 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265i	227 T C ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTTATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265h	80 T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTA GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265g	170 T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATTTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGCGCT

WI-7265f	231 T A ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGGTGT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAACCAAGCATATAGATGCATTAGTGATTTTGTATATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTTAAAGGAGTAAAGATTGGCCT
WI-7265e	227 T C ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGGTGT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCCT
WI-7265d	174 T A ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGGTGT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCCT
WI-7265c	170 T G ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGGTGT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCCT
WI-7265b	121 T G ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGGTGT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCATTGTGTA GTTTAAAGGAACCAAGCATATAGATGCATTAGTGATTTTGTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCCT
WI-7265a	80 T A ---	---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGGTGT TTCCAGTATGTTTATTTGCCACCAAAAGTAAATGCAATTTACCCATTCTGTGGTTCATTGTGTA GTTTAAAGGAACCAAGCATATAGATGCATTAGTGATTTTGTATATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGGCCT
WI-7281b	183 C ---	---	---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAAGTCTGGCCAGCCTGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTTGGCAAAAACGGAGTCCGCGAGGCCGAG GTGTTGTGAAGACCACCTCGTTCTGTGGTGGGGTCTCTGCAAGAAGGCCTCCTC
WI-7281	171 C A ---	---	---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAAGTCTGGCCAGCCTGCCCTGCAGGTCTCCCATGAAGGCCA OCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTTGGCAAAAACGGAGTCCGCGAGGCCG CAGGTGTTGTGAAGACCACCTCGTTCTGTGGTGGGGTCTCTGCAAGAAGGCCT

WI-7282b	159	G C ---	---	TGTCACCTGGCACATTCATTTCTCAGTTGAAAGAGAAAAATTTGAAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTTGGTAGGGTGAGTGTTCCACTCAAAATATGTCAACTNNNNNNNT AGGCCCTTCATAAAACCAAACTG/CJTAGCAAGATGCAAATGCATGGCAAATCTGTCGGTCTCCA GTTGGTTATCTGAATAGTGTACCAATTCACCAAGACAGTGTGAGATTGG
WI-7292	92	T C ---	---	CTTGATTACTCCACTGAGGTGGGAGCATCTCCAGTGCTCCCCAATTATATCTCCCCACTCCACTAC TCTCTCCCTCCACTTCATTTTCCT/CJTTGTCTCTCTCTCTAATTCAGTGTTTGGAGGCCTGACTTG GGGACAAAGTATTATGATATTATGCTGTTTCTCTCTCCCAATAGAAGAATAAGTCATGGAGCC TGAAGGGTGCCTAGTTGACTTACTGACAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A G ---	---	AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTG/TGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTG A/GJCGGTAGTAACATAATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCA ATCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301e	94	T G ---	---	AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTG/TGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTG TGACGGTAGTAACATAATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301d	138	A G ---	---	AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTG CGGTJ/A/GJTAACATAATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301c	211	A C ---	---	AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTG CGGTAGTAACATAATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC/CJCATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301b	182	C T ---	---	AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTG CGGTAGTAACATAATGGTGGTGGGAACTATAATGATTTTGGAAATTAC/CJTAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301	88	G T ---	---	AACTATGGCAGTGGTCTGTTATAGTAGTAGAGGCGGGTATGGTGGTGACAGGATATGGAA ACCAAGGTGGTGATATGGTGGTGGTGGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTG TGACGGTAGTAACATAATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGGCAGTTTGGTGAAGAAGCTCGGGCAG

WI-7301	205 A C ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGGGCGGTATGGTGGTGGACCAAGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGGTGGAGGATATGATGGTTACATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACATATGATTTTGGAAATTACAGTGGACACAGCAATCA AATTACITGGACACATGAAGGGGCGAGTTTGGTGGAAAGCTCGGGCAG
WI-7314c	49 G A ---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA[G]ATTTGTCTACCTCACTG AGAGGAACAGAAAGGATATTGCTTCTTTTGCAGCAGTGAATAAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACACGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAAGGA CAGAAATGTGAGTCTACCTTTATTTTTTATTAAACAAAACTTGTTTTT
WI-7314b	49 G A ---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA[G]ATTTGTCTACCTCACTG AGAGGAACAGAAAGGATATTGCTTCTTTTGCAGCAGTGAATAAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACACGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAAGGA CAGAAATGTGAGTCTACCTTTATTTTTTATTAAACAAAACTTGTTTTT
WI-7314	36 A G ---	---	CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAA[G]TTTGGGAGGTCAAGTTGTTCTACCTCACTG AGAGGAACAGAAAGGATATTGCTTCTTTTGCAGCAGTGAATAAAGTCAATTAATAAACTTCCCAGG ATTTCTTTGGACCCAGGAACACGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAAGGA CAGAAATGTGAGTCTACCTTTATTTTTTATTAAACAAAACTTGTTTTT
WI-7321b	199 C T ---	---	ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGGTGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAGTCTGACAGTCAAGGGAAGTCTTTGGCATCCAGGGCCTCCA GTCACTCACTGCCATACATTAGAAATGAGACAATCAAAAGNNNNNNNAGGGTGGCACACCCATC[C T]GTTGCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199 C T ---	---	ACTCAGGGAAGGGATGCCCCATTAAAGTGACAAAAGGGTGGGGTGTGGGCACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAGTCTGACAGTCAAGGGAAGTCTTTGGCATCCAGGGCCTCCA GTCACTCACTGCCATACATTAGAAATGAGACAATCAAAAGNNNNNNNAGGGTGGCACACCCATC[C T]GTTGCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248 A C ---	---	AGACATTTCTCGCTTCCCTGAAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCOCTGGC TCCAGTGAACACTGGGCACATGCTCAGGCTACTATAGTCCAGAAGTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAATAATCTGAATTTTGGGATTTTCAAAGATAATATTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGCAGCAACCTATAAATCA[AC]CA
WI-7338c	221 A G ---	---	CTCTTTCTCAGCACATTGATGGCAACTAGATTACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTTTTACACAC[AC]ATATACACACAGACATCAGAAAAATTTCTGTT

WI-7338b	125	A C ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAG CTAGTGTTCTCTCTTACACACATATACACACAGACATCAGAAAATTCGT
WI-7338	125	A C ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATGGCAAAAGGTGCTTT[A/C]CCTTG AGCCATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAG CTAGTGTTCTCTCTTACACACATATACACACAGACATCAGAAAATTCGT
WI-7338	221	A G ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACCTCACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATGGCAAAAGGTGCTTTACCTTGAGC CATTATTTGTGTGAGAGAACAAAGAAACAGAAATCAATATATAAAATTCAAAGACTATCTGCAGCTA GTGTGTTCTCTTACACAC[A/G]TATACACACAGACATCAGAAAATTCGT
WI-7384c	146	T A ---	---	CCTATGTCATGAATGCTAGGGGGCCAGGGAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATACTTTAAATACCATTAATACATTTGATTTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAAATTCCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384b	146	T A ---	---	CCTATGTCATGAATGCTAGGGGGCCAGGGAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATACTTTAAATACCATTAATACATTTGATTTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAAATTCCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384	145	T A ---	---	CCTATGTCATGAATGCTAGGGGGCCAGGGAACAAAATTTTAAATAATAAAATTCACCATAG CAATACAGAAATACTTTAAATACCATTAATACATTTGATTTTCATTGTGAACAGGTATTTCTTCA CAGATCTCATTTT[A/J]AAAATTCCTTAATGATTATTTTATTACTTACTGTTGTTTAAAGGGATGTTA TTTTAAGCATATACCATACACTTAAGAAATTTGAGCAGAAATTTAAAAAGAA
WI-7388c	106	A T ---	---	TGAAATCCTGGGTCCTTGGCCTGCTGAGTGGTTATTTTACTTTGCCCTCCACCTTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACT[A/J]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGTCGTCTGCCAAGAACTTTTCCCCAAAGATGTTATGTTG
WI-7388b	106	A T ---	---	TGAAATCCTGGGTCCTTGGCCTGCTGAGTGGTTATTTTACTTTGCCCTCCACCTTTTT TGAGATCCATCCTTTATCAAGAAGCTGAAGCGACT[A/J]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTGA CTTGTCGTCTGCCAAGAACTTTTCCCCAAAGATGTTATGTTG

WI-7388	94 T A ---	---	TGAAATCCTGGGTCTCTGGCCTGCTGCTAGCTGGTTATTTTACTTTGCCCCCTCCCCACCTTTT TGAGATCCATCCTTTTATCAAGAAGT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCACTTATAAGCATTGCAACAAGTTACCTCTATTTTCCACAAGGCTCTCGGGATTGTGTTGA CTTGCTGTGCTCCAAGAACCTTTCCCCCAAGATGIGTATAGTATTGG
WI-7438	64 A G ---	---	TTAGATTTTAATTGGCAACCAAGCACTCACTGCCACCATCCACTGCAGATCTNCTATTCTCGG[A/G] GTTGATATGACAAGGAACCCCTATTGGAACCAAGTCTTCAGATTGNCATGTGCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTCTACTGTAAACATAGTTTGCTGCTGTTGTTA TTGAAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152 T C ---	---	CCATGATCCCCTCCTCTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAAACCCCTGATAGCACTGTCTGAATTGCCAGGAGCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAATGTTTTGACA
WI-7454	152 T C ---	---	CCATGATCCCCTCCTCTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAAACCCCTGATAGCACTGTCTGAATTGCCAGGAGCTCCAAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTTGTTTAAAGTTATTTCTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAATGTTTTGACA
WI-7464c	177 G C ---	---	AATTTGAAATCTGAAAAAAGTGCAATAGCAGAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAAATGCACTAAATTAATTTTAAATTTCCCTATGTA CAACAGAGCCACAGCACAGAGGGTGGGCATAGCAGTTGCCA[G/C]CCAGAGAGGCTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTTCAACCAATTAT
WI-7464b	168 C A ---	---	AATTTGAAATCTGAAAAAAGTGCAATAGCAGAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAAATGCACTAAATTAATTTTAAATTTCCCTATGTA CAACAGAGCCACAGCACAGAGGGTGGGCATAGC[A/G]AGTTGCCAGCCAGAGAGGCTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTTCAACCAATTAT
WI-7464a	103 C A ---	---	AATTTGAAATCTGAAAAAAGTGCAATAGCAGAGAGAAATGACACTTATCCAAATAAATAAATTGT CCATTTTCACTCAGTCCATCTTAACCATGTACAAATG[C/A]ACTAAATTAATTTTAAATTTCCCTAT GTACAACAGAGCCACAGCACAGAGGGTGGGCATAGCAGTTGCCAGCCAGAGAGGCTTCACTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGAGCAACGTTTCAACCAATTAT
WI-7499b	134 T G ---	---	CAATTTCAATCCAACTAGTCTGNTGCCTAAACCATCCAGACAACTCCACTTCGAAGGTTTTTA AATGCAATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGTTCTTTGAATGCTTCAT /GJTATAGTCCTCTTCAATTTAGCAATCAGTGAGGCAATACATGGCATCATGCCCTTTTTTAGGA ACTCTGTACAAAAATCCCTTTTGAAATATAAATTTTGGAATGAGTGATGA

WI-7499a	33 A G ---			CAATTCTCAATCCAACCTAGTCTGNTGCTTAA/GJCCATTCCAGACAACTTCCACTTGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGGACACATCACGTTCTTTGAATGCTTC ATTATAGTCCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGAA CTCTGTACAAAAATCCCTTTGAAAATATAAAATTTTGGAATGAGTGATGA
WI-7506b	118 A C ---			TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAACAAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGAGTAGTCTGGTCTGATTGCCTAGC/CJGGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAATATTTAAATATTGGACCACCTTGTCTACCATCCCTACCCACT
WI-7506	118 A C ---			TGGGAATAGTAAGAGAAAGATGGAAAGGTGACCAAAACAAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGAGTAGTCTGGTCTGATTGCCTAGC/CJGGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAATATTTAAATATTGGACCACCTTGTCTACCATCCCTACCCACT
WI-7534b	143 C T ---			TGTGAATCTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGGTTCTTGATGTGTGGAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATTCGGGTGATAGAAATGCT AAATTGTC/JGTGAAATAGGTTAGAAATTTTCTTAAATATGTTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAATGGATTGGTGGTGTATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C ---			TGTGAATCTTAGCTCTGGAAGGTGTTATGCCCTTTCGGGGTTCTTGATGTGTGGAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCCGTGGAACACATTCGGGTGATAGAAATGCT /CJAAATTTGTCGTGAAATAGGTTAGAAATTTTCTTAAATATGTTTTCTTATTCGTGAAAAATTCGG AGAGTGTCTGCTAAATGGATTGGTGGTGTATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ---			GGGAAAGAATAAAATAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGAAAGCCCACTTGAAGGAAGAAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTCTTTCCTTGAAGAACCCAGCTTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7543	162 G A ---			GGGAAAGAATAAAATAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGAAAGCCCACTTGAAGGAAGAAAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTCTTTCCTTGAAGAACCCAGCTTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7555c	60 T C ---			GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGT/CJCTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGCAATTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGGAAGTAAAAATGAAGTCTGACTAGAAATTTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCAATTTTGAATTCAG

WI-7555b	60	T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTC
				AAAAGAAAGTGGTATGTTGTGTGATCAGCACTAAGTCTGCATTCCTGTTAAAGCCACTGGGTC
				ATAAGAAGGGAAGTAAATAAGAGTCTGACTAGAAATCTATTGCAGAGGCCAAAGTACATTTAGT
				ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTGAATTTTCAG
WI-7555	60	T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTC
				AAAAGAAAGTGGTATGTTGTGTGATCAGCACTAAGTCTGCATTCCTGTTAAAGCCACTGGGTC
				ATAAGAAGGGAAGTAAATAAGAGTCTGACTAGAAATCTATTGCAGAGGCCAAAGTACATTTAGT
				ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTGAATTTTCAG
WI-7567b	290	G T ---	---	TGAGCCATCACTAGAAAGAACCCATTTTCAACTGCTTTGAAACTTGCTGGGTCGTGAGCATGAT
				GGGAATAGGAGACAGGGTAGGAAAGGGCGCTACTCTTCAGGGTCTAAAGATCAAGTGGGCTTGG
				ATCGTAAAGCTGGCTGCTGTTGATGCTATTTATGCAAGTTAGGGTCTATGATTTAGGATGCGCTAC
				TCTTCAGGGCTAAAGATCAAGTGGGCTTGATCGCTAAGCTGGCTCTGTTT
WI-7569b	63	T C ---	---	AATGATCCCTTTTCGGTCCAAACAGGAACCTGACTGGGCGAGTGAAGGAAGGATGGCATTC
				AGCGTTATGTGTAATAAACAAAGTATCTGTATGACAAACCGGATCGTTTGCAGTAAGTGAATCCAT
				TGCGACATTGTGAAGGCTTAAATGAGTTAGTGGGAATAGCGTTGTTATCGCCTTGGGTTTAAATT
				ATTTGATGAGTTCACCTTGATCATGCGCTACCGGAGGAGAGGAGTTTG
WI-7574c	216	A G ---	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTTCTCTGTTTGTGTTGCCAAGGCCAAAC
				TCCACTCTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCTCAGTGAATCATTTTG
				TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAATGAGTTGGACAGTTCCTG
				ATAGCCCAGGGCAGTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574b	216	A G ---	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTTCTCTGTTTGTGTTGCCAAGGCCAAAC
				TCCACTCTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCTCAGTGAATCATTTTG
				TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAATGAGTTGGACAGTTCCTG
				ATAGCCCAGGGCAGTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7574	216	A G ---	---	GCCACAGCAGAATGGAGCGGTGTGAGGAAGGTCCCTTTTCTCTGTTTGTGTTGCCAAGGCCAAAC
				TCCACTCTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCTCAGTGAATCATTTTG
				TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAATGAGTTGGACAGTTCCTG
				ATAGCCCAGGGCAGTCTGCTGGGCTGACCACGTTACTCATCCCCGTTA
WI-7576c	168	A T ---	---	AATGATGATGATAATGATGATGACGACGACAACGATGATGCTTGTAAACAAGAAACATAAGAGAGC
				CTTGGTTTCATCAGTTAAAAAATTTTGAAGGCGGTACTAGTTCAGACACTTTGGAAGTTTGTGT
				TCTGTTTGTAAAAACTGGCATCTGACACAAAAAATGTTGTTGAAGGCTTATTCTACATTTTCACTAC
				TTTGTAAAGTGAGAGACAAAGCAAGCAANNNNNNNNAAAAAATAAAAC

WI-7576b	168 A T ---	---	AATGATGATGATAATGATGATGACGACGACAACGATGCTTGTAACAAGAAAAACATAAGAGAGCCTTGGTTCATCAGTGTTAAAAATTTTGAAGGCGGTACTAGTTCAGACACTTTTGGAAAGTTTGCTCTGTTGTTAAACTGGCATCTGACACAAAAA[A/T]GTTGAAGGCCCTATTCTACATTTCCACCTACTCTTGTAAAGTGAGAGACAAGAAGCAAAANNNNNNNNNAAAAAGAAAAATAAAAC
WI-7577g	77 T C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAAATAATGCA[T/C]CAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAATAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAAGCATCAAAAGTGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577p	50 G C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAAATAATGTCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAATAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAAGCATCAAAAGTGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577o	157 G A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAAATAATGTCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAATAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAAGCATCAAAAGTGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577n	48 A G ---	---	AACCATGTTCCCTTCTCTTAGCACCACAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAAATAATGTCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAATAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAAGCATCAAAAGTGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577m	84 G A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAAATAATGTCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAATAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAAGCATCAAAAGTGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577i	93 T C ---	---	AACCATGTTCCCTTCTCTTAGCACCACAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAAATAATGTCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAATAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAAGCATCAAAAGTGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577k	154 C A ---	---	AACCATGTTCCCTTCTCTTAGCACCACAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAAATAATGTCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTGTAGTAACAGTAGGAGTTAATAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAAGCATCAAAAGTGAGATATGTTAACTATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC

WI-7577i	117	A G ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTA[G/C]ACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577i	77	T C ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577h	50	G C ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577g	157	G A ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577f	48	A G ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577e	84	G A ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577d	93	T C ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577c	154	C A ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAA[G/C]JGTTTGCCTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGCATCAAAAGTGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577b	117	A G ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTGCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTCTGAGGGTTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAGTGAGATATGTTAACTAT TGTAATATGGCCCTGTTATACATGACACTCTTCTGAATTGACTGATTTTC
WI-7577	107	G A ---	---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTGCTTTCCCTTTAA AAATATGCATCAAAATCGTCTCATTACTTTCTCTGAG/GJAGTTTGTAAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTTACACGTAGGAAAGAGAGAGCATCAAAGTGAGATATGTTAACTAT TGTAATATGGCCCTGTTATACATGACACTCTTCTGAATTGACTGATTTTC
WI-7619q	106	C G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAAGGCGCAATGGGGTCAATCCCTCCCTAACGAGACTTC/GTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150	T C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAAGGCGCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTC TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228	A G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAAGGCGCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTC CGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619n	237	G C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAAGGCGCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTC CGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99	C T ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAAGGCGCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTC TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189	T A ---	---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAGCAAGAC AGAGAAAGGCGCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTC TCTCGCTTTCTTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGTATCCGCTCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTAC ATGGCAGGAAGAAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619j	206 T G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTAC ATGGCAGGAAGAAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCT CTCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	106 C G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619h	150 T C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619g	228 A G ---	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCT CGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619f	237 G C ---	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCT CGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619e	99 C T ---	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG TGGCAGGAAGAAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619d	189 T A ---	---	---	ACAAGGCGACTTGAAGAGGACGCGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAGAC AGAGAAGGGCCCAATGGGTATCCCTCCCTAACGAGACTCTGTGCTGGGGGTGCTAATTACATGG CAGGAAGAAATGGGGCCTTAAGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTCCCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619c	90 C G ---			ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACACAAGAC AGAGAAGGGCCCAATGGGGTCATCC[C]GCTCCCTAACGAGACTCTCTGCTGGGGTGTCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---			ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT CGCTTGTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---			ACAAGGCGACTTGAAGAGGACGCGAGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACACAAGAC AGAGAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTCTGCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGGCTCTAAGGGGAGTGGGGTGTCTCTCCCTTTTCCATCTTTTCCCTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---			CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGC[N/G]TTAAACCATCATGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCCCTTGGACTGTTC
WI-7626c	155 C T ---			CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATGACCAAAATGTGCCA TACTAATGATGAGCAATTTAG[C/T]ACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCCCTTGGACTGTTC
WI-7626b	28 T A ---			CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAG TAATCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCCCTTGGACTGTTC
WI-7626	144 T C ---			CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAAACCATCATGACCAAAATGTGCCA TACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTATTTATAGTAACCAATTTTCCCTTGGACTGTTC
WI-7689c	134 A G ---			TCCCAACCCGCTGATCTCAGGGTCTCTGCTGCCGCCCAACCAAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGCAAAAGGTTGTTCTTAAAJA /GJTAAGGGCAGAGTCACACTGGGCGAGCTGATACAAATTTGACACTGTGTAAAGAGAGGCTTAAT GATAATATTGGTGGCCACAAATAAAATGGATTATTAGAAATTTATATGAC

WI-7689b	134	A G ---	---	---	TCCCATACCGCTGATTCACAGGCTCTGCTGCCGCCCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGAAAGGTGTTCTCTAAAG /GTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGGTGGCCACAAATAAATGGATTTATTAGAATTCATATGAC
WI-7689	121	G A ---	---	---	TCCATAACCGCTGATTCACAGGCTCTGCTGCCGCCCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCCAGAAAGGTGTTCTCTAA AATAAGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGAGCTTAAT GATAATATTGGTGGCCACAAATAAATGGATTTATTAGAATTCATATGAC
WI-7690	45	G A ---	---	---	TGGAGAACATTCAATCTTCCGTCACATTATCATCAATGAAGATTG/AJCACTGAGATCCAGAGAGG CTGGATGACTTGTCAAGTTCAACAGCATGGTAGTGCAAGAGAGGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCCACAAAGCTCAGTAGGAGGATGTTCCAGTGATGAGGCCACCCAGGAAGCAC AGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACAACCTGTCAGTTCATCC
WI-7703b	164	T C ---	---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGTTTACATTTGGAACAAGTCAGTCATTGATATGATTCAAA TGTCATAAACCAAACTGATGTAAGTAAAT/CJGGTCTCTCATTGTTTATTAACTCTAAATTCCT TTCATTTTAGGGGTAGCATTTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7703	156	T C ---	---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGTTTACATTTGGAACAAGTCAGTCATTGATATGATTCAAA TGTCATAAACCAAACTGATGTC/AAGTAAATGGTCTCTCATTGTTTATTAACTCTAAATTCCT TTCATTTTAGGGGTAGCATTTGTTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7743e	106	C A ---	---	---	TTAAATGAGTGTGTTGTACCCGTTGGGATTTGGGAAGACTGTGGCTGGCCTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGAGGTCAGGAGAG GAGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCC
WI-7743d	275	C T ---	---	---	TTAAATGAGTGTGTTGTACCCGTTGGGATTTGGGAAGACTGTGGCTGGCCTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGAGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCCAACG
WI-7743e	106	C A ---	---	---	TTAAATGAGTGTGTTGTACCCGTTGGGATTTGGGAAGACTGTGGCTGGCCTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATTCGTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGAGGTCAGGAGAG GAGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCAGCTCTCAGCC

WI-7765b	126	G C	---	---	ACAGGGCCCTTTGGCAGGTGCAGCCCCACCTGCTTTGACCTGCTCCCTTCATGCATGGAATTCCTCTCATCTGGAAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTATGG[G/C]TTAGGGAACATTCCTCCTTGAGTCAAAAAATCTCAATTCCTCCCTATCTTGCACCCCTCATGCTGTGTGACTCAAACCAATCACTGAACCTTGTGAGCCCTGTAATAAAGGTCGGA
WI-7773b	237	C G	---	---	TTAATTTACTGATCCAGCAAGACCAATCAATTGTATCAGATTATTTTAAGTTTTATCCGTAGTTTTGATAAAGATTTCCCTATTCCTGTTCTGTGAGAGAACCTAATAAGTCTACTTTGCCATTAAAGGCACTAGGGTTCATGTCTTTTACCCTTTNNNNNNNNNTGTAAGTCTAGTTACCTACTTTTCTTTGATTTTCGACGTTTGACTAGCCATCTCAAGCA[C/G]TTTCGACGTTTGA
WI-7774b	170	T C	---	---	TGCAACCTCTTTTCGTGATGGGAGCCTGCTGGTCAGCACTCCAGTAGCGAGAGACGCGACCCAGAATCAGATCCCAGCTTCGGCAATTTGATCAGACCAACAGTGTCTTCCCGGGGAGGAAACACTTTTAAATACCCCTTTGCAGGACCACTTTAATCTGTTT[C/G]ATACCTTGTCTTATTAAATGAGCGACTTAAATGATTGAAAATAATGCTGCTCTTAGTAGCAAGTAAATGTGCTTGTCT
WI-7785c	165	G	---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGATTAGAAATAATTTATTGCTGTAATCTGTAATGCAATGGAATGAACTGTCTCCCCATTTGCTCTATGAAACTGCACATTGGTCATTGTAATANNNNNNNNNNNGCCAAAGGTAATCCAATTATTATCACATTTACCAATAATTTATTTGTCCATTGATGATTTATTTGTAAATGTATCTTGGTGTGC
WI-7785b	165	G	---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGATTAGAAATAATTTATTGCTGTAATCTGTAATGCAATGGAATGAACTGTCTCCCCATTTGCTCTATGAAACTGCACATTGGTCATTGTAATANNNNNNNNNNNGCCAAAGGTAATCCAATTATTATTCACATTTACCAATAATTTATTTGTCCATTGATGATTTATTTGTAAATGTATCTTGGTGTGC
WI-7785	156	T	---	---	GCAGAGACCTTCCAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGATTAGAAATAATTTATTGCTGTAATCTGTAATGCAATGGAATGAACTGTCTCCCCATTTGCTCTATGAAACTGCACATTGGTCATTGTAATANNN- /TJNNNNNNNGCCAAAGGCTAATCCAATTATTATTATTCACATTTACCATAATTTATTTGTCCATTGATGATTTATTTGTAAATGTATCTTGGTGTGC
WI-7789c	84	G A	---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGCGCACCATCTTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGACCCAAAATGTGAATGAAGCTAATGTGAATGTGAATGAGTGAAGTCCCTTCAAGCCCGCTGCGCTAGGATATGCCCTCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7789b	84	G A	---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGCGCACCATCTTACAGAGACTCTCCCTGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGACCCAAAATGTGAATGAAGCTAATGTGAATGTGAATGAGTGAAGTCCCTTCAAGCCCGCTGCGCTAGGATATGCCCTCTGGTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT

WI-7789	73 GA ---	---	---	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGCGACCATCTTACAGAGACTCTCCG TGACG[G/A]TGGAAATTTAAGTTTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GCCCTCCTGGTGACTCGGGGGCTGTCTCAGACGACTAGCCAGGACCCCATCT
WI-7790b	190 CT ---	---	---	AATTGTCAGTCACCTCTTCAAAACCTTACAGTCCTTCTTAAGGTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCTATGTGCTTATGTGTAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[C/TT]TCTATACITTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACITTAAC
WI-7790	190 CT ---	---	---	AATTGTCAGTCACCTCTTCAAAACCTTACAGTCCTTCTTAAGGTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCTATGTGCTTATGTGTAGCTTTTACTTTTATGG TGTGATTAAATGGTGATCAAGGTAGGAAAAGTTGTGTTCTATTTCTTGAACCTC[C/TT]TCTATACITTT AAGTACTCTATTTTAAACACTATCTGCAAACTCAGGACACITTAAC
WI-7795b	81 CA ---	---	---	CAGATGTTCTGGTAACTGATTGCTGGCAACACAGATTCCTTGGCTCATATTTCTTTCTCAT CTTGATGATGAT[C/A]GTGATCATCAAGAAATTTAATGATTAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTTCTCCAGAAAATCTCCTTGAGGAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTCTAAATTTGAAAATAAATCTG
WI-7795	81 CA ---	---	---	CAGATGTTCTGGTAACTGATTGCTGGCAACACAGATTCCTTGGCTCATATTTCTTTCTCAT CTTGATGATGAT[C/A]GTGATCATCAAGAAATTTAATGATTAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTTCTCCAGAAAATCTCCTTGAGGAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTCTAAATTTGAAAATAAATCTG
WI-7814c	41 GA ---	---	---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCACTC TGCTTTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814b	41 GA ---	---	---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCACTC TGCTTTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814	28 GA ---	---	---	TTCTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCACTC TGCTTTGTGTTTCCACAGCCTGCAAGTTGAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA

WI-7830d	150 C T	---			GCAGAAATAGTCACATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/T]TAATGTACACATTGCAATTTGATAAAATTAATTTGTTGTTCCCTTTG AGGTTGATCGTGTGTTGTTTGTGTCACATTTTACTTTTTGCGGTGGA
WI-7830c	54 G A	---			GCAGAAATAGTCACATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCAATTTGATAAAATTAATTTGTTGTTCCCTTTG AGGTTGATCGTGTGTTGTTTGTGTCACATTTTACTTTTTGCGGTGGA
WI-7830b	134 G A	---			GCAGAAATAGTCACATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGAAC G/AJATCCATAACTTTAGTCTTAATGTACACATTGCAATTTGATAAAATTAATTTGTTGTTCCCTTTG AGGTTGATCGTGTGTTGTTTGTGTCACATTTTACTTTTTGCGGTGGA
WI-7830	44 A G	---			GCAGAAATAGTCACATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTCTGTTAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCAATTTGATAAAATTAATTTGTTGTTCCCTTTG AGGTTGATCGTGTGTTGTTTGTGTCACATTTTACTTTTTGCGGTGGA
WI-7865e	25 C T	---			CCACTTCTATCTGATTTTCCCAG[C/T]AAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTAGGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865d	191 C T	---			CCACTTCTATCTGATTTTCCCAG[C/T]AAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG ATGCTACTCATAAGATTTAGGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTAC[C/T]GAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865c	25 C T	---			CCACTTCTATCTGATTTTCCCAG[C/T]AAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTAGGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA
WI-7865b	191 C T	---			CCACTTCTATCTGATTTTCCCAG[C/T]AAATGAGGAGGCAATCTAGTCTTCCACAAAACATCTA ATCTAAATGGAGAGATGAATCATTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG ATGCTACTCATAAGATTTAGGGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTAC[C/T]GAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTCACCCAGTAAACCCAAA

WI-7865	25 C T ---	---	CCACTTCCTATCTGATTTTCCACAG[C]/AAATGAGGCAGGCAATTTCTAGTCTTCCACAAAACATCTA GCCATCTAAATGGAGAGATGAATCATTTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTACATAAGATTTCAAGGTGCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCTTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865	191 C T ---	---	CCACTTCCTATCTGATTTTCCACAGCAATGAGGCAGGCAATTTCTAGTCTTCCACAAAACATCTAGCC ATCTAAATGGAGAGATGAATCATTTCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTTCAAGGTGCTTCCAACTGAAATCTCAATGTTCTCAGT[C]/TGA AAAAC CTGAAATCACATGCTTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7867c	92 A C ---	---	TTCAAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACTTCCAGCTCAGCTCAGTCCCC CTAACAAATTACCTGTCAAGAGG[C]/GAGTGCAGCTCAGGTGGATTTAATGTGGGTTAATATGGC CTGTTGAGTTTAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7867b	92 A C ---	---	TTCAAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCACTTCCAGCTCAGCTCAGTCCCC CTAACAAATTACCTGTCAAGAGG[C]/GAGTGCAGCTCAGGTGGATTTAATGTGGGTTAATATGGC CTGTTGAGTTTAATGTTAATGTTGATTTCTTTAAGTAACCATTTCTGTTCTTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTTGGATTAAAGG
WI-7868c	173 C T ---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT CACCCAACTGTCTCCCTGTGATCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCA[C]/TTAGAGGCCAGAAAAATGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCTAATGCTAGAT
WI-7868b	173 C T ---	---	TTGATCGATCTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCCGGGCTTT /CTCACCCAACTGTCTCCCTGTGATCTCCATCAGGGCCAGATCTTCCACGTCTCCATCTCAGTACAC AATCATTTAATATTTCCCTGTCTTACCCCTATTCAAGCACTAGAGGCCAGAAAAATGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCTAATGCTAGAT
WI-7868	66 T C ---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGG GTGGGGTGGCGGGAATCC[C]/AATTTATCAGACTCTGTAATGAATATAAATGTTTACTCAGAGGA GCTGCAAAATGCTGCAAAAATGAAATCCAAATGAGCACTAGAAATTTTAAACATCATTTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGAGACCACCTAATATCAATTG
WI-7870b	85 T C ---	---	

WI-7870	76 C T ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGG GTGGGGTGG[C/7]GGGAATCCTATTATCAGACTCTGTAATGAATATAAATGTTTTACTCAGAGGAG CTGCAAAATGGCTGCAAAAATGAAATCCAATGAGCACTAGAAATTTAAACATCATTTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C ---	---	---	TTAGGTCTATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGCGGGGCCAGGGCCTCT GGCTCCCTGCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATTTGAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGCTCTCCAGAGCACAAAG
WI-7889b	54 C ---	---	---	TTAGGTCTATGCCACTCCCCAGGAGCAGCTGGCACTGACAGCTGGGGGGGCGCTCTCCCCCTG CAGCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACTACAGGACTGGCGGGGCCAGGGCCTCT GGCTCCCTGCCAATCCTCCCTGGAGAAAGGACATGGGAATGAATTTGAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGCTCTCCAGAGCACAAAG
WI-7894c	142 A G ---	---	---	AGCCACCCCCAAATATAACTGTATCCAGAAGCTGTATGCTCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATGTTTGTGAATTTATTTGCGTATAC ATTATC[A/G]ATGTAAATTTGCAATTTTATTGAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---	---	---	AGCCACCCCCAAATATAACTGTATCCAGAAGCTGTATGCTCTGTTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGCTCTATGTTTGTGAATTTATTTGCGTATAC ATTATC[A/G]ATGTAAATTTGCAATTTTATTGAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/7]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/7]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/7]CCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATCTCTCAGATTTGAACCCAGTGAAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC

WI-7900d	128 C T ---				GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TAACA AAATGCATTGATCATGAATAGAGCCCATGCTAGAAGTACATTCCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T ---				GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/TCCTGCCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGAGCCCATGCTAGAAGTACATTCCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T ---				GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TAACA AAATGCATTGATCATGAATAGAGCCCATGCTAGAAGTACATTCCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900c	84 C T ---				GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/TCCTGCCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGAGCCCATGCTAGAAGTACATTCCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128 C T ---				GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TAACA AAATGCATTGATCATGAATAGAGCCCATGCTAGAAGTACATTCCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84 C T ---				GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/TCCTGCCATTGAACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGAGCCCATGCTAGAAGTACATTCCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33 C T ---				AGACTTAGGTACAAATTGCTCCCCCTTTTATATA/C/TAAGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCCCTTGGTGGGGTGGTGGTATTGGGGCAGCGCCCGTGGTGGT CACACAGTGGCTCTGCATGCTCTGTGCATACAGACAGGTAACCTAGTCTCT
WI-7901b	33 C T ---				AGACTTAGGTACAAATTGCTCCCCCTTTTATATA/C/TAAGACACACACAGGACACATATATTAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCCCTTGGTGGGGTGGTGGTATTGGGGCAGCGCCCGTGGTGGT CACTCAGTGGCTCTGCATGCTCTGTGCATACAGACAGGTAACCTAGTCTCT

WI-7901	33 C T ---	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATA[C/T]AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTATTAACACATGGTAAGAC CCTTTTAAACAACTCCAGCCCTTGGTTGGGTCGCTGGTTATGGGCGAGCGCGGTGGTGGT CACTCAGTCGCTCGCATGCTCTCTGTCATACAGACAGGTAACTAGTCT
WI-7901	271 T G ---	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATAACAGACACACAGGACACATATATTAAACAGATT GTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTATTAACACATGGTAAGACCCCT TTTAAACAACTCCAGCCCTTGGTTGGGTCGCTGGTTATGGGCGAGCGCGGTGGTGGTGCAC TCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACTAGTCTGTGT
WI-7926c	150 C A ---	---	---	CATTCCGCATCTGTCAACAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTTAGCAAAGTGATACAAACACAGTATTTGGGAATGCCCTTCATT TACAATGCAATACCTA[C/A]ATTTTAACTCTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926b	28 A T ---	---	---	CATTCCGCATCTGTCAACAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGC ACTTTGGAGATCAGAAAATTCATATTTAGCAAAGTGATACAAACACAGTATTTGGGAATGCCCTTC ATTACAATGCAATACCTA[C/A]ATTTTAACTCTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926	150 C A ---	---	---	CATTCCGCATCTGTCAACAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCAC TTGGAGATCAGAAAATTCATATTTAGCAAAGTGATACAAACACAGTATTTGGGAATGCCCTTCATT TACAATGCAATACCTA[C/A]ATTTTAACTCTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7947b	203 G T ---	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACCAATAGCAGCCAGCCACAGGCCAGGTCCTGT GCTATCACAGGTCACCTCTTTACAGTTAGAAACACACAGCCAGGCCACAGATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGCTCAATTCAAATCCATAGATTTGGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGGAGCCCGAGTCTGCCACCTG
WI-7947	203 G T ---	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACCAATAGCAGCCAGCCACAGGCCAGGTCCTGT GCTATCACAGGTCACCTCTTTACAGTTAGAAACACACAGCCAGGCCACAGATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGCTCAATTCAAATCCATAGATTTGGAAGCCACA GA[G/T]TCTCTCCCTGGAGCAGCAGACTATGGGAGCCCGAGTCTGCCACCTG
WI-7963b	145 T C ---	---	---	CATGTGCTGCATGAAGAGCTAATTTAAAAAGCAAGTAAGACTAATTTTAAAAATAAAAAATGCC ACAAATTTTCATTTCTCCCTTCTAAGTATTACAATGGAGTTTATCTCTGCTTAAAGGTGGAAGAAAT TGAGTGAATGA[T/C]JAATTTTGTAAATTTAGGATAAGATCCCAAGTTATTTCCCCAACTCTTGTTC CCATAAAGTTAGGCATGAGGAGGAGCACTCATTAAGGCAGAAAGACGGGAAAA

[illegible]

WI-8021b	57	C T ---	---	---	ACAACTCAGAAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATCTCATCTGGAAA[C/T]GATCCC ACGTCCTTAGAACCTTACCACAGAGTTTCTTGTAGTGATCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCCTTTCACITTTGAGATCTTTCTTTTGGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8021	57	C T ---	---	---	ACAATCTCAGAAAGGACTGTGCAAGTCAATGAGTCGCTTGTGAATCTCATCTGGAAA[C/T]GATCCC ACGTCCTTAGAACCTTACCACAGAGTTTCTTGTAGTGATCTCAAAGTCTTGGTAGGCATTCGA ACTGGTCCTTTCACITTTGAGATCTTTCTTTTGGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8024c	206	A G ---	---	---	CTGAAAATTTACTATGCTCTCCACAAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTATCATCAACAAACCAATTTACGCCGCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCTGCTCAGTACACAAAGGAAAGAGC
WI-8024b	206	A G ---	---	---	CTGAAAATTTACTATGCTCTCCACAAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTATCATCAACAAACCAATTTACGCCGCTCTAGCCTCTAA TTCCC[A/G]CTCTAGAACAGCTGGCCCTGGTCTGCTCAGTACACAAAGGAAAGAGC
WI-8077	167	A G ---	---	---	GAATGAGCCTTCTAGCGCCGAGGGACCTGCTGCTGTTGTCGCTGCACATGCTTCTATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNATCTGCCCAAACCTCCTTCT AAGGAGCTGGGTGTCATGCCCTACAAACC[A/G]TAAATTCATCAGATGGATTTTATTTAAGCTT GTGATTTGAGACTTACTTTCCAAATCTGACTCTGGCATAACAAGGGAAAAA
WI-8118f	114	G C ---	---	---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAAATGAGCTTGT[G/C]TTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40	A G ---	---	---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAAATGAGCTTGT[G/C]TTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118	T G ---	---	---	TCTAGGTTTAAATCAAAGCAATTTGCANTTTGGATTTTGGATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAAATGAGCTTGT[G/C]TTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---			TCTAGGTTTATCAAAAGCAATTTGCANITTTGGATTTTGGAAATGA/C/TCACTCCCTTGCTAAGGAAGC TATGACTTTCATGCTGTGGAACTGGCAATACAGAATGAGCTGTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTTCGATTTCCCTGCTCCTCTATTCCTTCCT AAAATCAGACTCATTTGTACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---			TCTAGGTTTATCAAAAGCAATTTGCANITTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAAC/T/CJGGCAATACAGAATGAGCTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTTCGATTTCCCTGCTCCTCTATTCCTTCCT AAAATCAGACTCATTTGTACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCGGCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCACACA TTTATGGAGGGTTGCCCTGAAGAGAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8171c	46 A G ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACIAGTGGCAGCAGGGCCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCAC ACATTTATGGAGGGTTGCCCTGAAGAGAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46 A G ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACIAGTGGCAGCAGGGCCTCGGG AAGAGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCAC ACATTTATGGAGGGTTGCCCTGAAGAGAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298 T C ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCGGCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTCTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCACACA TTTATGGAGGGTTGCCCTGAAGAGAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85 G C ---			GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGGCCATTGCAATTTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGG[G/C]AGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAAGACACTGTCCAATAGAATTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCACT
WI-8314	78 C G ---			GAGGGGAAATGACATCTGGAGATCTAGGTATGTGGGCCATTGCAATTTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGG[G/C]TAAAGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAAAGACACTGTCCAATAGAATTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAAACCACT

WI-8321	178	G A ---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTTATACTGAGTCTCTGAGAAG TCCCCTTAGATAATAGTGCACATTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATTCTTTCTA TTTTGCTATGGTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8321	178	G A ---	---	TTTTAAATATGCCCGTTTAGAGCAGACACAGTCACATAAAAGTTAAAAAGTTACAATGTGTCCAG TGTATATACCCAGGNAATCCATTCTTGGTACTTTTCAAGAGCTGCTGTTATACTGAGTCTCTGAGAAG TCCCCTTAGATAATAGTGCACATTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATTCTTTCTA TTTTGCTATGGTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTGGC
WI-8332b	123	A C ---	---	TATGTAACCTTTTACAGTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCAAAGCCAGCTTTTCCCTTCCCTGTCAGCCTTAGA/A/CJACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCAGCAATGCCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C ---	---	TATGTAACCTTTTACAGTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCAAAGCCAGCTTTTCCCTTCCCTGTCAGCCTTAGA/A/CJACTAAGTAG CAGTACTGTTTGGTGTGTTGTTTCTTCCCAGCAATGCCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGGTNTCCGGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T C ---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCTCAGGAAGCTTATAATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGGAGAAAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACTNTACAGGCCCCCTCCTCCACACAGTGTTGGG
WI-8378	308	T C ---	---	TGCGGGCTTAACAGGAAGCATGACTGGGAGGCTCAGGAAGCTTATAATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGGAGAAAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCAATCACTNTACAGGCCCCCTCCTCCACACAGTGTTGGG
WI-8426	184	T G ---	---	TTTAGCACATATTTAGCATTAAAGCCTCAAACGATACAGCAATATGTTACATTCTCTGTGAAAAACAG TTGTTGTAGACTGTTAANNNNNNNNAAATGTAACCTCGACCTTGCCCTAATAGGATTTGACCNITAA GAGGNTTCTTTGCTGTGGANGGGGTGGCTTGTCTGAACCTCCATTCTGTG/GJGCTTGTAGCTGGTG AGGCTGGGAGTATGGANGGNCOCGGGGCCCTTGGGNATNGNATTCAGTGAG
WI-8450b	61	C A ---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTTC/AJCA TCTTCTATCTTAGTCCAGTTTGTGTTTCAATCCCAATATACCAATTTCCATTGTTATTTTAAGA AAAAACCTTCCAGTTATGTCAGAAACTATGATTTAGCTTACCCCTCCACTCCCACTCCCAACACTAC AGAGAGGATGGGAGTGAATATGAGCAGTACAGAGTCTTAATGCAATTCAT

WI-8450g	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCACACTCCAT CTTCTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTCCCAAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A G ---			CAAGGAAGCTGTCAGTCTTCAAACTTTCAAAAGAGTTACAAAATACGTAATTTTTTAAAGJCTA CAATTCGAAGATTAGCATCCAAACCTACAAACATGATGTACATTCGTACACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATAGTTGTGAAAACCTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105 A T ---				CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCAATTTT[A/J]NNNNNNNNCCCTTGCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---				CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAAT[C/J]ATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATCAATTTTNNNNNNNNCCCTTGCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---				CTTCCTCCTCCAAAATCTACATGAATACCTTGAAGACAATATAACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCAATTTT[A/J]NNNNNNNNCCCTTGCTTATTCACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---				AATAACATGTTATGAAACAAGCTGTTACAAGTAGTAGGTAGTAGACTTAATTTTGATAAAAAAAT TAAAAAGCATTA/GJAACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATAATTTCTCCCTTGTTTGTCTTTTAAAAAACATTATTTCTGAAAAAATAA ATCAGAAAAACATGATCGTGGAGAGAAATTATTA
WI-9438	77 A G ---				ACAGAAATGACCTTTATTTGTTGTAATAAGCCTGTTTAACTTTTGATACAAAAGTAACATTTTAGTA CAGAAAAATCCAGTCTGTCAGCTCAGTACCTGT[C/J]TGTCACACTGTACCATCTCAGTCCCACTCT GCCTGTAACCTTAGAAAAACAGCCCTACCCCAAGAGGCTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTGTACCTGTAAAACAAAG
WI-9439b	101 C T ---				ACAGAAATGACCTTTATTTGTTGTAATAAGCCTGTTTAACTTTTGATACAAAAGTAACATTTTAGTA CAGAAAAAT[C/J]CCAGTCTGTCAGCTCAGTACCTGTCTGTGCACACTGTACCATCTCAGTCCCACTCT GCCTGTAACCTTAGAAAAACAGCCCTACCCCAAGAGGCTCTGCGAGTTAATACCTTGAGAATAGTCTA CAGTTTTTCATAGTTTGTCTGAGCTAGAAAACCTGTACCTGTAAAACAAAG
WI-9439a	76 C T ---				GAAGGCTTGATTAGGGAGGNTTTATTTGATGTGNAACCTTACCATTCACACTATAAAGANCATTTA TAAAAAAAT[C/J]CCTCTAAAGNGACACATGCCCAAAATGACCANGNCATAGCAAAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTGTGNNCCCTACINTTATCACTGTGTCTTCTGCTTTTGTGTACCTTA TGNGAACTGCACACTAICTGTGGCAATATGT
WI-9446b	75 T C ---				

WI-9446	75	T C	---	---	GAAGGCTTGATTAAAGGGAGGNTTATTTGATGTNAACCTACCAATCCATAGACTATAAAGANCATTA TAAAAAAAT/CJCCCTCTAAAGNGACACATGCCCAAATGACCCANGNCATAAGCAAACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTTGNCCCTTACTTATATCACTGTGCTCTTCTGTCTTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185	A	---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAAATGGTATATATACATTTTTTT GAGATAATTATCTAGATTCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCITTAATTAATCAAAAGTATGTTAATGTCACTT GGAATTTACATGGAAAAGCCCAACAAATAACTAAAACTTGACTAATGAAG
WI-9497	185	A	---	---	ATTAAATGTCAAGGTTTCATGTTTACATTTTCTTATATCAAGTACAAATGGTATATATACATTTTTTT GAGATAATTATCTAGATTCAGGCTTCTCTAGATGTAAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCITTAATTAATCAAAAGTATGTTAATGTCACTT GGAATTTACATGGAAAAGCCCAACAAATAACTAAAACTTGACTAATGAAG
WI-9523b	193	C A	---	---	GTGAAAAAGTTTCTATTCCATCCATCATACATAGATTGTCTAAGGATCATTTTGGAGAATGTG CAGCATTCAGAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCACA GACTCAGACAAATTACAAACTATTTTCAGCCATGATCTATGGTGATTTTCCACACATTGTATC/AJAGTG AAAGCTTTCAGCTTGGAACTTGTCAAGGCAGACTGCATGCACATATAT
WI-9523a	47	G A	---	---	GTGAAAAAGTTTCTATTCCATCCATCATACAAATAGATTGTCTAAGGATCATTTTGGAGAAT GTGAGCATTCAGAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAAGTACGTGCA CAGACTCAGACAAATTACAAACTATTTTCAGCCATGATCTATGGTGATTTTCCACACATTGTACAGTGA AAGCTCTTCAGCTTGGAACTTGTCAAGGCAGACTGCATGCACATATAT
WI-9554	202	T C	---	---	AAAAACACAAAGTTTCATACATCACAAAAAACCTTCCATTATAACACAGAGTGATTATTACCAGAC AAGCATCAGTGATGATAGTACTGCCCTTTCAGTTTGTATTGTACAAATGCTGTAGATAATGCAGCCCATG CAATACACCCCAAGAACACTAGAGTCTCTACACCCCAAGTACAAATATGATAAAGCAGCCCTCTCTGCAAGTG GT/CJGCTGGATACCACTAAGAAAGTCTACTGCAGCCCATGTTGGTTATGATTTT
WI-9555	97	G A	---	---	CCAAAAGCCAAACCATTTCATATGATGGATTTCATAAACAATTTATTGATCCTTTTGGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAACG/AJCTTGAAAAATCAATTTCAAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAATACAGGTAAGTATTCAG GGNTAAATGGTACAAAAAAGGCTGTAACTCTTTTNCITTCACATTGATCACA
WI-9625b	172	A T	---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAAATCTGCAAGTAAATCAATCATTTT TAAACATAGCTACCATATATTTGTATCTNCCTCTGGGAAAAAATCTTGGAAAAAATAACACGCACA TAAGTATCATAACTGAGGGTTGGGACAAGTTACTCT/AJGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTAAAAAACAACACTGCACAAATCTTTTC

WI-9625	172 A T ---			TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAAATAGCTACCATATATTGTATCTNCTCCTGGGAAAAAATCTTGGAAAAAATCAACACGCACA TAAGTATCATAAAGTGGGTTGGACAAGTTACTTCT[AT]GTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTAATAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---			TTTTCTGAGATCAAGAGCTACATTTTGGTAGTGTACTACTATACCTTTTTCATCCTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTGTAAACAGTGTATTGCTAGACCTAAAAATCCAAAGCT TACAACT[CT]GTCTTTACCTGATACATTTATCCATTTACTTTTCAATTTGGAATTTTAAAAATGTTA ACTTAATACGTCCTTTTACAGATGCTCCTGCTTTTGTAAATGTGTTT
WI-9676n	114 A G ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCA[AG]GATGTGGCTTTCCTGGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676m	184 G T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGC[GT]CATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676l	84 A C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676k	202 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA C[TT]CAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676j	92 C T ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC CCCATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTCCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676i	173 T C ---			GGCCACTGTCCAAAGTCTGTACAGTCTCCTCCATATGGCAAAGATGAAGAAAAATGGCAATCTTTTA GGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTTCCTGGCC ATTTCACTCAAGGCATCTTCAGCAACCCACATGGCTT[CT]CCCTCTGTGGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9676h	134	C A	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCCTGCCCCQ C/AJATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG C/TJAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676f	184	G T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676e	173	T C	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCCTGCCCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676d	134	C A	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676c	114	A G	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676b	92	C T	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676a	84	A C	---			GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATGGCAATCTTTTAA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAAATGCAGAGCAAGATGGCTTTCCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9738b	40	C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGGCCTGTGTA[C/A]ATTACAACATCATGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACCTTGCTGGAGCGGGTGTTTTCACATATGTGAGTATCTA TCCTTTTATTTCTGCTCCCTTATGTTGGTGGCACAATGCTGTGATGCTGTC
WI-9738	40	C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGGCCTGTGTA[C/A]ATTACAACATCATGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAAACACAGTAAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACCTTGCTGGAGCGGGTGTTTTCACATATGTGAGTATCTA TCCTTTTATTTCTGCTCCCTTATGTTGGTGGCACAATGCTGTGATGCTGTC
WI-9756	47	A ---	---	ACTGAAATGTAATGGCCCAAGGCCACCCAGGACCTTAAAAATCATAAGAAGTTAATCTGTGGAAAA GAGTAACTACAAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGTCCTTATCACATTTAGTC AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACTTCCACAAACACACAGAATATACACATTTTGGGAG ATTCCACTTAACCACTTGATCTTCACCTTTTATGATTTAAAACTCTCCGTGG
WI-9758	135	A G ---	---	GATGGTCCCTTAAGGATTTGCAATTGTTAATGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAAACTGGGAGAAITCAATCAAAGAAGAAATCTTGTTCGCAAGGTCAATTTTATACTATTTA A/A/GTAAAAAATCACTCTGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAACCGTGGTTTCTAAAT ATTACG
WI-9778	127	G A ---	---	ATTTAAATCCAGGCAGCGGGGAAATGGATACITTTTCATATGCTCTGTACCCCAACTATAAACTTTTG GTTCTCATGCAACATTTTCATTTTGCTTCTCACTCAAGTACCACCTGATTTTACCAATT[G/A]CTCTC ATAATTGACTTTGCTACTGGAAGAAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTTGCCTCA AAGAATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	C A ---	---	TCCTCCCTTTGCTCTCTCATGCCACTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACATGCAGTTT[C/A]TGGATCCACCCAGGA CTCAAAAACACTAGGAATGGGAGAAAGAGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAAGTGGACTAAAGTTGAGGACCAGACATGGAAGTTGGCTTTGGC
WI-9841	101	A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAATGGCATGA TATGAAATTCCTATTTTGAATGAATAAAATATAC[A/G]TGTGTATGTATATATACCTTATTAACTT AGGATTATATACACACAATAAAACGCTGTGAAGGATAAACTAAGTTCTATCAGTGGGAAATGAGA TTGAAAAGAGGGGATGTGTACTTTGATATGCTGTG
WI-9880c	222	G A ---	---	GAACTAACACCTTTCTGCATGGATTTTCTTGATTGGCAGTTAACAATAAAATGTTATTAGATC ACTGGTCTCTGTGGGTTGAGTTTTTATGATATCTCTGTAGACCCCAAGGGAGGCTGTGA GTTGTTTTCTACATCCCTTGGACTATAAAGATCCCTCTTTTAAATATATTTTATAAGCACATGAA AATGGAATGAAATAATGA[G/A]TTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	C A ---	---	GAACTAACACCTTTCTGCATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTCTCTGTGTGGGTTGAGTTTTTATGATATCTCCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGAC[A]/ATATAAAGATCCTCTTTTAAATATATATTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T ---	---	GAACTAACACCTTTCTGCATGGATTTTCTTGATTATGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTCTCTGTGTGGGTTGAGTTTTTATGATATCTC[A]/CTGTAGACCCATAAGGGAGGCTG TGAGTTGTTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATATATATTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T ---	---	ACACTGCAGGCACCTCCAAATCCTNACAGACATATGCACTTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTTAAAAACAACGCCCCAGTTATCACAGTTTCTNTTTTGT[C]/CACC ATTTTCCATAACAAAAAGAGCTACACAAAATTNNGGGGGAGANACTCTCTTTGGAGACTGCACACATT TGCAGAGGGGTCTCATGAATAATGATTCAAA
FB25G10b	109	A G ---	---	TCCCTCAATGACAGATGAACATAATTTTCTCTTGGGTAAGAAATACTTTATGTCCATTGTGATTA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAAATGGA[A]/GJTGATTTTAGATCCTCCCCCAG TGACAAAGTAACTGAACCTGACCATATTTATACATAAAATGGAATGTAAGAACCCTATTTGGATATCC CGGAC
FB25G10	109	A G ---	---	TCCCTCAATGACAGATGAACATAATTTTCTCTTGGGTAAGAAATACTTTATGTCCATTGTGATTA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAAAATGGA[A]/GJTGATTTTAGATCCTCCCCCAG TGACAAAGTAACTGAACCTGACCATATTTATACATAAAATGGAATGTAAGAACCCTATTTGGATATCC CGGAC
IB3071	102	C A ---	---	ACAAGCGTGAACCTCCATAACAGTCAATGGTACAGTCAAAACATCAGTGTACAGAACACACAATTTA GATGAACCTGAAATTAAGNTAAATAAAATAAAAT[A]/CAATTTTCAGNAAACAAAAATCAAAAC ATTAAGGNTCCCTGNNTATTTCTTAAACCCTAATGAGATTTCACTGNGNCTCAAGTCATTTTGTAGTGA GGCATTACAAATATGACCCCTATTAAACCCAGTCTAGGGATTCTG
NIB551	161	C T ---	---	CGTCCCTTCCCTTTTGAGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATTTGGGTTGTCCC TACTGAGCTTGGGGCCAGGTGTGTACTTAGGAACCCCAATCCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGT[C]/TTTGACCACATACATGCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAACCCAAAGCTTGTCC
S72904	51	G T ---	---	AGCATAGAAAGTGATTTATATTTTAAATGGTTTTCAAGTGGAAAGTTCCTTTT[G]/JAATTTGCAGTTC ATTCTGGAAAAATCTTTTGAGTTAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTGCCTCAAAACCAAGTGCTGAACCTCCTCCCTTTCTGTCAATTTGGTTGTCTTTAAATA TTGCAAAAGTCCCTGATGCTAAACAGTATTTGGAGTGTTCAGTGTCTGTA

UTR-00481	115	CT				TATCTTTTATCCTGGGGCCACAGTCTTGATTATTCCTCTTGTGGTTAAAGACTGAATTTGTAAACC CATTGAGATAAATGGCAGTACCTTTAGGACACACACAAACACACAGAC/C/TACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33					CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37					GCTACTACCACGGCTGCTTCGTTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21					GCCATCAAAATTTCCCTTCACANTCAATACTGTGGAACAACAAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20					TGCTGGCTCACTTCCTCACANGCTGTATTACCTTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35					AAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGACC
ESTC110	23					AACTCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37					AAGGGACACAGTGTGCTGACAAGGTGACACTGAACANACAGTTTCCCTTAATTGTAAGCGGG CATCG
ESTC117	24					AATTGGCTCTTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCCTATCACAAATTTACAAAAAGC CTCCA
ESTC119	24					TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTT
ESTC122	34					GACAATAACAGCTAAGCTACTGACATATAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21					GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42					GCAGAGGCATCAGATAAGGCCCTCAGAAAGCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTGGAACCTGG
ESTC129	20					AGTCACCATGCCAGCCTAGNATGAGTTTAGTAAGATTTGGTTATGCTGGGGAG
ESTC13	46					GTGTATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAAA
ESTC130	49					GCCTGCTCACAAGGTAGACAAAAACATAAAATCTTCAGGAAAAATGAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCTTAGCAAAACNCTATGTTGTCAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTGGCTTCTGCTCCANAGTCTCTCTCCATGTGGCAACA
ESTC139	45	---	---	---	AGGACACAGCCTAAGGACATGAAGGTCAGAGTTTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCCATTGGTTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGCATGGTTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATAATCTATTTTATTCAATTTAAATC AAAGANACCATTCATTCTCCTAACAAACA
ESTC143	29	---	---	---	GTTTACGAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCCCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTCTTGACATGAGGTNGCTTTTTAGCAGCATTTTCGG
ESTC146	20	---	---	---	CATGTCAGGATAAGGAGCANACACAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	TCCTTGGTTGTCTACACAGACACTTAAGTACTGTATCGCTGNATGACGGGCTGTGGAGGCCCTG GGGTGGCTGGGCTGTGCTCTGAG
ESTC149	28	---	---	---	TCAGTTCATTATTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAAGTTCTTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAAACAAAGCACACANACTTATAGAATACCTTGGTTTAAAAAATTATTCATAATATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGGCCCCATTTTTTCTTTTAAATACAAATCTACTGGTGTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACTCAATCTCTACATACATACAGTNTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAAACTCATGAGCATTTTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGGAGCGCAAAACAAANCCCTGGCTGCTCGGGATGGAGCGGGGGGCTCA CCACCACTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGAGACTTCCTGAGGCACATCAGNTACGTTGGTCAATTTAGGGCACGGTCTGGTTCTGCA GCTTTGAAAGG

ESTC16	23	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCACAGTGATCATCACCCACAAGGACAGGTT TTCTAGCATTGCTGGTGCAGTGGGGCCCTGAGCTGGGNGCAGTCGGCAGTGTCACCTGGGCCCGTTTG GGACTGGGTTGA
ESTC160	38	---	---	---	CTCTCGTCCGTTTGCAAGTTGCTGTTTTCAGNTACACAGTCAGAGCTCCACAG TCATTCTCCATAGAATAATTGGTTTTGTAACANCGAATACAATCCAATATATAACATTAAAACAATCC GATACATACCA
ESTC162	36	---	---	---	GTCTCTGGTGCAGGAATCANTTGCTGGATTAGAGGAAGGTGCCGCCGTCIGTITTCCTCAIGACTT
ESTC164	31	---	---	---	CACCTCCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA TGGGTGGCTCTTTAAATACCTTCCATTATATTTCAAATTTTNCCTTATTCTATTAAAATACCTTTTAT TCTCTTATCCCATAAAAAGGCAACCAA
ESTC169	22	---	---	---	TCAGAACTGCCGACATCAGCATTGCTCNCNTGTACAGCTCCCTCCCTGCAGGGGCCCTGGGAGAC AACTGGACAAGA
ESTC176	23	---	---	---	TAGGGATTCCAAGTTGCCCTGGNTTAAATATAATACATATTCACAAAAATTTACACAGCTCATGCATAC CA
ESTC177	42	---	---	---	GCTTGACTAGCGAGGTACATCACAAATTTATAAGTGCCAGATNAGTGTAAATTGTCAATTCAGCTTG ATTTTCAACCTCA
ESTC18	29	---	---	---	ACCATGATTGCCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG TCTATTAAACAGGGTTATGTCACACCNTGTCAACCTCAAAACAGATGATACTCATCAGTTGCTCTCCAT CTTGC
ESTC181	21	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCAGACTCGTGATCA
ESTC186	43	---	---	---	TCCTCAAATACCACTTTCCCTAACTTATCAGTCTAGTAGCNITTTCAAAGGAGGAAAAATGGGTTAC CTTTCAGGGG
ESTC187	24	---	---	---	ATCTCCAGTGTCTGCTGCCCTCCTCCNGCAAAAGTCTCCACAAAGCACA
ESTC188	25	---	---	---	AAGATTAGGACAGACCGGTATAGTAGCTCTGNGGAACTCCAAGAACTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC189	27	---	---	---	TTTGGTGAAAAATCCCAATATATGAGTTTAAAAAATAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCTCTTTTGCTGCAACAG
ESTC196	42	---	---	---	
ESTC197	26	---	---	---	
ESTC20	33	---	---	---	
ESTC200	44	---	---	---	

ESTC201	35	---	---	---	---	TCCTACTTGGGTAGTCTTAGCAACATTTTTTAAANCCACATCCAACAGATTGGTT
ESTC202	22	---	---	---	---	CTGCTGGAGGGAGGACAGACGNCAGCGGCTGGGTGGCGCCGCCAGAAAGGCTGGCGTGGATGTT CGAGATGAGCC
ESTC203	27	---	---	---	---	ACACTTAACAGAGTTAAAAATATCCAAATNAAATTTACTGCAACTTTTGAGAAATTTTGTGCTAC AAGACACGTTGCA
ESTC208	43	---	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATAANAGCAATAACTATTGTTTAAAGC CTAAGAGTGAAAA
ESTC210	29	---	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAAGTGAAGTGAACGCTGACCTGIG
ESTC212	27	---	---	---	---	GGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGGCTTGGT TCAAGTC
ESTC214	21	---	---	---	---	CTCAGAGTCCCTCCTCTCANACCAGGGCAGGAGGAGTTAGGGAAT
ESTC216	49	---	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTTAAATTTAATCACAGGTATNTTAGATTGGTCAGAAAA CAAAAGACCA
ESTC217	28	---	---	---	---	TTTTGTCAGTAAATGAGCAATACACTGANTGGAAATCTGCATGATTAAATAACATTAACAAGTTCAT AAACACACCCCA
ESTC219	32	---	---	---	---	GTACACATCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG GCAAAGGAAGC
ESTC22	41	---	---	---	---	TCATTGAAGAAATATGGGTTTTTATCTTATTTCTAATTGNGAGAATGCTTAATGTCACAGGCTACA TAAGGCC
ESTC223	27	---	---	---	---	CTTCTGAAGCCCAAGAGAGGGGCGAGAANGTAGTCTTGATTTAAAAAACAGAAAGGGAGGAGGA
ESTC224	37	---	---	---	---	CGAAGGTAGATTTCCCTACATATTACAAAAATACACANAACACACACACACACACACA
ESTC225	20	---	---	---	---	TGCACTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGTCTCAGAAGGA ATGTGTAGGATCG
ESTC23	27	---	---	---	---	TTCTACTTTATTTTCATATTTCCACCACNATAACGACTCCTTTAATTTAACTAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	---	---	---	---	GCTTCCTCCACGAATTTGAAGACATATTGGCTGACCTGATACINTAAGGAGCAGGCCAGAAATTAAGA
ESTC231	24	---	---	---	---	CAAAAGGGTAGTCATATTCCCCCANCAACAGCATGATAAAATAATTCAAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNTTCTTCTCTATTCCTATAAAAAATAAAGGAAGCAGAAATCT GC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCNGGCCCTCAATTCATATTTTATCTTGAGCCGCTTGGTCAGGTTTGAT TCGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAAACAATATNTCAGTCGGTGATCATTTGTAATATACAATACAAAG CAATTTCTCTCAGA
ESTC33	25	---	---	---	AGCACTCCAGCTCCTTGACGTTGTNGGACCAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAGGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAATCATTATGCTGATGGAAAGAAACCATT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTTGAAGATCTTTTAAAAATATTTTGACTTGTCCCCCTTCAC
ESTC45	37	---	---	---	TTTGGAGGTTTGIGICTGGAGTTTGTCTTTGTAACTCTCATCATCGAGGCTATATATTA
ESTC50	56	---	---	---	CTGTCCGTGGTAGCCCTGCCGCTGTCCATGGCCAGGGAGCCACTGGTGGGANCCTGGGCAGATG TTTACCCTGT
ESTC56	45	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTGGCAGGAAGNAGTGGAGGGAAGGACACCA AGT
ESTC57	20	---	---	---	AAGTGGGCCCTCCAGTCCCTCTCTGGGCACAGATCCCACTGCTGCTC
ESTC59	38	---	---	---	GAAACACAAAAAGTGTGAGAAAAAACTTCTCAAAATNGTTCAGACTTCAGGAAAAATGATTTCC ACATGGTAAGGCC
ESTC6	27	---	---	---	TCTGCAGCACTTCACTACCAATGAGCNITTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATG TGGACTGAACCG
ESTC61	57	---	---	---	AGTGATTTGGCTAGGCGTGGTTCTCATCTGTGAATTCACAGCGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC63	20	---	---	---	ACAGACACAGCATCACACCANAGGCCACGGGAGGTGGGGAGACGACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC69	20	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCCTCAAGTTTAAATCCCCACACTTACTTACTGCTCATCCGT CACTTTCCGTAA
ESTC7	45	---	---	---	AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTCTCTGAGTTGCANGCACGATGGAGATTTGGACACT G

DWU-252	94 A G ---	---	AGTATACAAACATTTAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAGGCACCTTCATGTAAAGTGT CAGAAGGAGCTACAAAACCTACCTCA/GJTGAGCATGGTACTTGGCCTTTGGAGGAACAATCGGC TGCATTGAAGATCCAGCTGCTATTGATTTAAGCTTCCCTGTTGAATGACAAAGTATGTGGTTTGTGTA AT
DWU-330	85 C T ---	---	GAACATTCCTCTGCAGCACTTCACTACCAATGAGCATTAGCTACTTTTCAGAAATTTGAAGGAGAAAA TGCATTATGTGGACTGAA/CJTCGACTTTTCTAAAGCTCTGAACAAAAGCTTTCTTTCCCTTTTGCAA CAAGACAAAGCAAGCCACATTTTGCAATAGACAGATGACGGCTGCTCGAAGAACAATGTCAGAAA CTCGATGAATGTGTGATTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231 A G ---	---	GAAATGTTAATTGGCAGGTGAAAAGGTACAGATGTGCTGTAGCAGACCTTTGGTTTTAAAGAG AAGCATCATTTCCCAACAGGGCAACTGTAGAAAGCCAGCTGAAGAGTAAAGGAAAAGGTCTGAGG ACTGAGCCTGTGGCTGGCTGGAAAAGGTGAATGTTGAGGGCCCTTCACTCCATCACAAGAAAGTC ATTAGACGGTACCAATTCAGTGTCTGTTCCCTJAGJGCACTATTTCCCTCTGTGC
DWU-1537b	89 A G ---	---	CTCTTAACCTTCAGTTCCTCATCTATAAGAATAAGGGATTTCAGTTGTGATCACATAGCTCAGGTAATC CAGGACCAGAAACCCAGGAGCJAGJGGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAAACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52 C T ---	---	CTCTTAACCTTCAGTTCCTCATCTATAAGAATAAGGGATTTCAGTTGTGATCA/CJ/TATAGCTCAGGTA ATCCAGGACCAGAAACCCAGGAGCATGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAAACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196 C G ---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCCCTCTCTCCCTGTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTG/CJGJAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCCTCTGAGCTTGTCTC
ESTD-ADAA	184 G A ---	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCCCTCTCTCCCTGTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCCCTCJAGJGCACTGAGCTGCAGA CCCGCAGACCAACTCCTGAGCTTTCTGGGCCCTCTGAGCTTGTCTC
ESTD-ANT1	160 T C ---	---	TCTCTGTCTATTCTACTCCATTAGTTCAAGGTCAAGTGAAGAACTGGGGCAATTAACCAAGTAATTC TGGACTGCCCAACTCGGAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGGGTTACCTT TTTTTATGAGGACCCGAACCTGAGGCT/CJGAGCTCAGATGATCTGT
EST-10398 2b	168 A G ---	---	TGCCTGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTTCACTTTGGGGCTTGACTTTCCAAACACGGAGAAG CATTTGTTTTCTCGGGCCCAAGAAAGTATCTACCTAGJATAGTGTCTATTAGGCATTTG

EST10398	147	C T	---			TGCTGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGGGGCCATGGTA
2a	14	G C	---			AGATGCTGCCACCTCTTATCTACTTGATGATGTTACATTTGGGGCTTGACTTTCCAAACACGGAGAAG
ESTD-C7	14	G C	---			CATTGTTTCTTCTTGCGCCAAAGAGGTATCTACCAATAGTGTCTATTAGGCATTGG
ESTD-D4S95	90	T C	---			ATATCGTGGCCTTA[G/CTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-GPPK2L	38	G A	---			CTTTTCATGCACGATAGGCTTCTCTACTAATCACAGAATTTTGAGAAGAGCAAAACAACCTTCAAGG
ESTD-HRASb	82	A G	---			ATAATGGGGCAATCACCTTCTTTT[C/CTCTTTAGAGTCTACCCGG
ESTD-HRASa	37	C T	---			AGTCTTCATCTCGGGTGTCCAGGTAGATCCCTTTTACC[G/ACCGAGAAGTCTCGATATC
ESTD-NRAMP	81	A G	---			CTGGGCTGCCCCGACGAGCTGTGGCACCTGGACGGCGCGCCAGGCTCACCTCTATAGTGGGGTGG
ESTD-OTC	18	A G	---			TATTCGTCCACAAA[A/GTGCATCTGGATCAGCT
EST36751	36	C T	---			CTGGGCTGCCCCGACGAGCTGTGGCACCTGGACGG[C/T]GGCGCCAGGCTCACCTCTATAGTGGGG
7	36	C T	---			TCGTATTCGTCCACAAAATGCATCTGGATCAGCT
	18	A G	---			GGAGGCAGAGGTGGGAGGGGTCTGTCTGCTCCAGGTCCACAGACCAGAGAGGGGCTCAGTG
	36	C T	---			TATCCCCACCCCCA[A/GTGTGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
	18	A G	---			GTGACCTTCTCACCTTTAA[A/G]AAACTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC
	36	C T	---			AGATCTGAAATTTAGGATAAAACAGAAAGAGAGGTATGTAACA
	18	A G	---			CCAAGTCGTTCAATTTAGCTTTGCAGGTTTAACT[C/T]GATTACTTTTTCTATTCAAATCTCTGTA
	36	C T	---			AAATTGAAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
	109	A G	---			CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGATAAAGATCTGTCCCCAAACTTGTGGCTGAC
	121	C T	---			TTTATGGCTAAGAAAGTTTCACTGGATGCAATTAAACAAAT[A/G]TTTTACCTTTTGAACAAATAA
	109	A G	---			ATGAAGGATTGACCTGCTTCGCTCTGGAAGAGATACCGTACCGTCTGACGTTTTTGAACAAATACA
	121	C T	---			GATGCCCTCCCTTGTAGGAGTTTTCAGCCTCCTCTACCCCTA
	121	C T	---			GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGCTGAGAA
	121	C T	---			GATTGACAGGTTTCATGCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGA[C/T]GGGAGCCAGT
	121	C T	---			GTGGACAGCACCTTGGCTTTCAACACCTACGTCCTACTCCAAGGTAAGGCAAACTCTCTGCTGGCTC
	121	C T	---			TGGCCCTAGGACTTAGTATCC
	31	C T	---			GGGAGTGACAGCTAGACACCAAGGGGGGCT[C/T]TACAGCTGTGTCTCATGGAGGACAGGCTTCT
	31	C T	---			GCTCATTCGG
	180	A G	---			AATCCCAGCACCTTTAGGAGGCTGAGGAGGATATCACAGAGTTCAGGAGTTTGAGACCAGTCTGA
	180	A G	---			CCAACATGGTGAACCCCCATCTCTACTACAAAAATACAAAAATTAGCCAGGCATGGTGGTGCATGCTGT
	180	A G	---			AATCCCAGGAGGCTGAGGAGGAGAAATCGCTTGAACCTGGGAGGCG[A/G]AGGTTGTGGTGAAGCGGA
	180	A G	---			GATGGCACCATTCACCTCCAGCCTGGGCAACAAGAGTAAACTCTGCTCTC

ESTD-BC12	116 A G ---			AGCTGGATTATAACTCCTCTCTCTCTGGGGCCGCTGGGGTGGGAGCTGGGGCGAGAGTGCCGTTGGCCCCGTTGCTTTCTCTGGGAAGGATGGCGCACGCTGGGAGAAC/A/GGGGTACGACAACCCGGAGATAGTGAAGTACATCCATTATAAGCTGTGCGAGAGGGGTACGAGTGGATGCGGGAGATGTGGCGCGCGCCCCGGGGCGCCCCCGCACCGGCATCTCTCTCTCCCA
ESTD-BCR	69 C T ---			CACTGGCTGAGTGGACGATGACATTCAGAAACCATAGAGCCCCGGAGACTCATCTGCGCAAGA/GA/C/TCAAAGAGGTACGCTTCTGTTGCCCGGAAAGGGAGGCGAGGTGACAAAGCTAACTCTGCTCAAAATCAACCATCGGTGGACACTGTGTGGCTGCCATCTGCTCTGGCACA
ESTD-BCA1aa	119 C T ---			AAGAAGAGAAACTAGAAACAGTTAAAGTGTC TAATAATGCTGAAGACCCCAAGATCTCATGTATAAGTGAGAAAGGGTTTTGCAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCAC/TJTGGTACCTGGTACTGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAAACA GAACCAATAAAT
ESTD-BCA1bb	139 A G ---			ACTAAATGTAGAAAAATCTGCTAGAGGAAACCTTTGAGGAACATTCATGTCACTGAAAAAGAGAAATGGGAAATGAGAACATTCCAAAGTACAGTGAGCACAATTAGCCGTATAACATTAGAGAAAAATGTTTAAAGIAG/GAGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCA GTATTAAATGAAA
ESTD-BCA1cc	126 A G ---			ATGCATCTCAGGTTTCTGAGACACCTGATGACCTGTAGATGATGTGTAATAAAGGAAGATAC TAGTTTCTGCTGAAATGACATTAAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGA/A/GIAGGA GAGCTTAGCAGGAGTCTAGCCCTTACCCATACACATTTGGCTCAGGGTTACCGGAAGAGGGGCCA AGAAATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
EST512120	122 A C ---			ATCCTGAGCTCGCCAAATAGCTTCTGGTTCTACTCTCTCTTCCACAAGCCCCCAATTCACATTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCCTTTGTGCTCCCACCAATACA/A/C/JAAAGGCCCTCTCTACATCT
ESTD-C1R	40 A G ---			ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCTCTCCCTTGA/GJATTGCTCCGGGAAGCACATTCAATCAA
ESTD-C1R	40 A G ---			ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCTCTCCCTTGA/GJATTGCTCCGGGAAGCACATTCAATCAA
ESTD-C6	31 A C ---			CCCAGTCAGTTGGGGGACAGCCATGCACCTG/A/CJGCCTCTGGTAGCCCTTCAACCATGCATTCCTCATCTAAGCTCTGCAAAAT
EST201182	119 C ---			GTCCGAATCCTCCTCTGAAAGTGGCGGGTTTAATCTGCTCATGACGTCGGGCTGTGGTCCAGCTGAGGTGAGGGGCTTGAAGCTGGGAGTGGGGTTTAGGGACGGGGTCTCTGCTGCATCTCAAGCTCTGAGAGCAAACTCCCTTGAAGCTGGGAGTGGGGTTTAGGGACGGGGTCTCTGCGTGCATCTCAAGCTCTGAGA
EST530186	67 A G ---			ACAATCCAGGTACACATTCAGAAAGAGGAGGGGTGGTCAGTGAGCCTGGGTAGGTCCAGTAATCCCAIAG/GGATTACGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTCT

ESTD- CB22	119 C T ---	---	GGCAAGTTTTATTGATAGAGAGGAAATCAAAATATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAATGGGCAGTGCCAAACCCATAGGG[C/T]GGATACAAAAG ACAGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCT AGTAACATAATTGCTTCATTATGGTCTTCCCGGCTTCTCTCACACAC
ESTD- CB23	136 C ---	---	TAGAACATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTCCCGGCTTCTCTCACACATACAGAGAGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAAAACGTGTTCCCAACCCGA GGTCGTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCCAAA
ESTD- CB24	145 A ---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTGGTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACACCAAAAG GCCACACTGGTATGCCTGCCACAGGCTTCTACCCCGACACGTTGAGCTGGTGGTGAATGG GAAGGAGTGCACAGTGGGTGAGCAGACAGACCCGCGCCCTCAAGGAG
ESTD- CB25	146 A G ---	---	GTTTTCTTCAGACTGTGGCTCACCTCCGTAAGTGAGTCTCTCTTTCTCTCTATCTTCGCCGTC TCTGCTCTCGAACCCAGGCGCATGGAGAAATCCAGGACACAGGGCGGTGAGGAGGCCAGACCTG TGCACAGGTAAG[C/T]CTACATGCTCTGTTCTTGTCAACAGAGTCTTACCAGCAAGGGTCTGCTGCC ACCATCTCTATGAGATCTTGTAGGGAAGGCCACCTTGTATGCCGTG
ESTD- CB27	125 C T ---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGGCTGTTGCATTCAGGAGTGTCTGTGGAGTCTGCTCATCACTGAC[C/T]ATCTTC TGATTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCAATGCT GCTTCTCTGTTTCATCTGATGGAAGTCTCAAAACACCATTTCCATACC
ESTD- D4S338	59 A T ---	---	TTTTCTGTTTACCTTGTTTCAGATCTTCAGAGGAATCCCTATATATGGCAGGTATATGA[T/AT]GTA TTTCTTAAACAATAAACTTGAAAGTCCAAAATTACTCCTTGATCCATGGACTGCAGAAATAAATGTTA TTTTAGCTGTCAGAAAACAATACTAATCTTGCATATGTTTCATCAGAGCCCTTGGTGACCAGGTGTA TTGCCAATAAGCAGTAATAATTTGAGAGGAATCTTGTTTTCAATGCAGTAG
ESTD- CYP2D6	61 A G ---	---	CAGGCCAGCGTGGTCGAGGTGGTCACCATCCCGGCAGAGAACAAGTACGCCACCCTATGC[A/G]CA GGTCTCATCATTTGAAGCTGCTCTCAGGGTTCCCTTGGCCCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	40 A C ---	---	AAAAAACAATTTAACACCTTTTCAATCATATACACCAATA/GIATTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAAATTAATTTGCAATCTAAATGTCATAACTGATTAATGCAAGTTCAACAG ACAACCTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATGCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T ---	---	CATCCCCAAGCCCATCTCTTAGCCACTGGCATTTTGGCCGCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGGAAGGCTCCTCTGGGGCGGTG GGGTGTGTGGCTATGTGGTGTCTGTGTAGAG[C/T]GGGGGCTTTGGTTTCAGTTGCACATATGGGTT ATTGCAGATTGCTTTGCTTTCCACCTTGAGCGAGCCCTC

ESTD- D17S33a	75 C T ---	---	CATCCCCAGCCCATCTTAGCCACTGGCATTTTGGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCTACACATCCAGGGGCGCCCTACCCCTTGTAGTCCATGGAAAGGCTCCTCTGGGGCG GTGGGGTGTGGCTATGTGGTCTGTGTAGACGGGGCTTGGTTTCAGTTGCACATATTGCGTT ATTGCAGATTGCTTGTCTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---	---	TTTGAGACCACCCTGGCCAAATGGCGAAATCACATCTTACCAAAATACAAAATTAGCTGGGTGT GGTGTACATGCCTATCGTAATCCAGCTACATCGGAGGCTGAGCAGGAGAAATGCTTGAACCCQA /GJGAGGCAGAGCTTGCAGTGAGCCAAAGATCACACCCTGCACTTACAGCCCTGGGTGACACAGTGGA GACTCTGTCTCAA
ESTD- D3S11	44 G ---	---	AACTGATTAGAACCTGAAATACATAATTTTATCTGAAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAAATCCAATAAAGTACACTGTATAAAGAAATTTAACAGAAATATCATTTGT TTATCAAACCTATTTATCATTATTTATTGGTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---	---	AGGTTCCACATTATTGCTGATGTTTGGCTGATGTTTCQJGJGAGCCCTTGATGTCATCTGTATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTGTTATTATTCAGGTT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAAACGTACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCC AGAAGTGAACATACACTGCTCTAGAACCCAGAGTACATAGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTGGGAAGGATGCCTTGGT
ESTD- D3S2a	248 G ---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAAAACGTACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCC AGAAGTGAACATACACTGCTCTAGAACCCAGAGTACATAGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTGGGAAGGATGCCTTGGT
ESTD- D7S399	83 A G ---	---	TGAATCTTAATTGCTATCTACAAAATGTATAATCCTGAACTGTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCJAGTCTCTCTCTACATCATCTTTCACAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DMb	146 A C ---	---	GTGGGGACACCGAGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCTCCACT TCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGGAGAGGAGGGAGTGGGAGGGAGACA GAAATGCTGATTJACJCTGTGGTGAGAACCAAGAACTTCTGGCTGTGGGTAGGGGCAGCTGCTTCCAAG ACCTCTGATTGTAGGAAGGGAGCAGCAGAGCGAGAGAGAGAGT
ESTD-DMa	66 C G ---	---	GTGGGGACACCGAGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCTCCACJ GTTTCCATGGGTGTGGGCTGGGACCTCACTGTCCCTGGGGAGAGGAGGGAGTGGGAGGGAGAGA CAGAACTGCTGATTATCTGTGTGGAGAACCAAGAACTTCTGGCTGTGGGTAGGGGCAGCTGCTTCCAAGA CCTCTGATTGTAGGAAGGGAGCAGCAGAGCGAGAGAGAGAGAGT

ESTD- DRD1	154 C T ---				TCCCAGCCCTATCGGTCAATTTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAG ACAAAACGGTCAGCACCCCAACCTGAACCTCGCAGATGAATCTGCCACACATGCTCATCCCAAAGCT AGAGGAGATTGCTCTGGGIC/TJCGCTATTAGAAACTAAGGTAC
ESTD- DRD2	144 C ---				TCTGCCTTTGGTGCAGGAGGCTGCCCCGGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGAGACCCGGTACAGCCCCATCCACCCAGCCACACAGCTGACTCTCCCCGACCCG TCCCACACGGTCTCCACAGCACTCCGACAGCCCCCGCCAAACCCAGAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---				AAGCATGGCCAGGATGAGCGGCAGTAGGAGAGGGCATAGTAGGCATGTGGCGGCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAAGTGGC/TJACTCAGCTGGCTCAGAGATGCC ATAGCCAGAGGGAGGTGCGTGATGCCAAGGGCTCTCTGTGAGGAGA
ESTD- ERBB2	93 C T ---				TCTTCAGGATCCGCATCTCGCCTGGTTGGGCATGCTCCGCTAGGTGTCAGCGGCTCCACAGCTGG GGTGAGGGGGTGGTGGTCAAGTGC/TJGGGGCCGGTGCAGACCCACGCGGGCTGGGAGGACTTCA CCCCGCTCACTCCGTTTCTGACGACGTCTCCGCATCGTGTACT
ESTD- ETS2	43 A G ---				ACTCACAGTGTCTTTAAGTGAATAATGGTCGAGAAAGAGGACCACTA/GJGGAAGCCGTCCTGGCGCCTG GCAGTCGGTGGGACGGGATGTTCTGGCTGTTTGAGATTCAAAGGAGCGAGCATGTGTGGACACA CACAGACTATTTTAGATTTCTTTGCCTTTTGCACCCAGGACAGCAAAATGCAAAAACCTCTTTGAG AGGTAGGAGGGTGGGAAGGAACAACCATGTCTTTCAGAAGTATGTTG
ESTD-F9	111 A G ---				AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTAGATTATGCCCA TGCTCCATTTGAGTTAATATTTGTGTAAGTATGATGTTTAA/GJGTCAAACCTCATTTTTTTTCC ATAGGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144 A ---				CTTCCTATGGGATTGACTTTATTTCTCCTCAATGTCTTACCTTTTACAGGTGTTAATATAGTGAAGA GAAGCTTGAGCTCATGACAAATTTGAAGCTGACAAATACACAAGAAAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAACATTTGAAGTTGTTTTGAACCTTGGTGTCACTTTAATTAACACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GDDH	200 C G ---				CGCAGACCGGTGAGTGGGTGGGAGTGTGAGGGAAGGAGGGAACCTGGGGGTTAGGGACT TTCCGGGTGACTTTCCGTTCTGTGCTTGCAGAGAAAGGGGGGAGAACACAGAGCCAACTGGCTAA GTGAAGGACCTCTGTGTCGACCGTGTGTTCTGTGCTGCCCTGTTCAGCTGTCTGTCTGCCGAGT/C GJACTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	88 A G ---				GTTTTATGCATGGCAGCTCTAATGACAGGATGGTACCCCTGCTGAGGCCACTCTCTGGTCACTGAC AACCACAGGCCCTCTCAGGA/GJACAGTAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAAATGCCGAGCGGCGCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTC ACCTGCAGCCTAATTACTCAAAGCTGTCCCCAGGTACAG

EST34088 2	62 A T ---	---	GTGGGGCAACAGTGGGAGAGAAAGGGCCAGGGTATAAAAGGGGGCCCAAGAGACCGGCTC(A/T) AGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ---	---	GACCTGAGTACCTCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCCAC(A/G)GGCATCA TTGAAACCAAGTTTCCGTCAAGACTTGAATTCAGGTAAGTGCATGGTTCCCTAGG
ESTD-HT2	154 G ---	---	GGCTAAATTTCCGAGCAACTTTCATAGACTGTTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTACAGAGAGATAAAAGGATAAACCTGGGTTTTCTGTGC TTTGCTCTTCACATCCCTGGGGAGTTAATAGTGCATTTTTCAAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTTCAAACAGACACACCTT
ESTD-HT5	149 C ---	---	AACACAAAGCCCGCAGGAGAAITGAACTCGGACCCCTGGTTTACAAGACCAGTCTTAACCCCT GAGCTATGGAGCCCTGCTGCTGTTGTTTTCTCCCTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGCTACCGAATAGGATGTTAGCTTGAGTAAATCCAGGATATTCCTCTACAAATGAAA ACATTTTCGTGCTCTGTAATCCCTCGAAAGGTTCT
EST37382 5	124 A G ---	---	CTGAGAAACAAATTGGCAAAATAAGGAATTTGGCACTCCCAACCCCTCTTCTCTCCCTTGGGA CTTTGAGTCAAAATTGGCTGGACTTGAGTCCCTGAACAGCAAGAGAAAGAG(A/G)CCCCAGA AATCAAGGTGGGCACGTCGCTACCGCCATCTCCCTTCTACAGGGAATTTTCAGGGTAAACT ACCCAGTGGAGCCCGCTCATTCACGCTCTTGGCAGGAGTG(C/T)CTGGGAGAAAGGAAGATG TTCCAGGCAACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ---	---	TTTACTATTCAATGGATACAGAAITTTGGGAGTCACTATATTCCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTTGCCTACATTTGTGTGAGTGACGGGCAGTGGTGATCCGAGAGTGTGGTGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACITTCACAAAATACTAATAACGGAGTTGAATATAAAACCCCA
ESTD-IL1A	110 A G ---	---	CAAAGTAAGCACCCAATAAATGTTAGCTATTACTATCATATTATTATTATTTATTTTITG AGATGGAGTCTGGCTCTGTCAACCCAGGCTGGAGTGCAGTGGC(A/G)CAATCTCGGCTCACTGCAAGCT CTGCCTCCTGGGTTCAATGCCATTTCTCTGCTGCTCCGAGTACGCTCCGAGTACAGGCACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTGTAGTACAGAGGAGTTCAACCGT
ESTD-IL1B	99 A G ---	---	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTCTCTGCCCTC(A/G)GGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T ---	---	TCCAGGGTGGCTGGACCCAGGCCCGCAGCTCTGCAGCAGGGAGGACGTGGCTGGCTCGTGAAGCATG TGGGGGTGAGCCAGGGGCCCAAGGCAAGGACCTGCGCTTACAGCTGCCTCAGCCCTGCCTGT(C/A) TCCAGATCACTGTCTTCTGCCATGGCCCTGTGGATGGCTCTGCCCTGCTGGGGCTGCTGGCC CTCTGGGGACCTGACCCAGCCGAGCCCTTTGTGAACCAACACCTGTGGG

EST45311 0	151 C T ---			GCCTCCTCTCTCCAAATTCGTGCTCCCTATAGTTTTCTCTATTAAAGTGAACATACATGCATCTTTTAGT GGATAGATGCACACACAAACACAAAGCCATTATGGGAAGGATCCACGTGTGGCCATATTGTAACA CATTTTCTGTCAAATC/TACCTCTTTCAATTTAACAGCCCTTATTCAATGGCCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258 8	80 A G ---			TGCCCCATCAGCGGGCCGAGACATGGCTGCCACAGCTCTGAGGATGTACCAAAATTAACCAGAAAT CCAGTTATTTCC/GJCCCTCAAATGACAGCCATGGCCGGCGGGTCTCTGGGGCTGCTCGGG GGACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGCGGTTTCCGTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3	26 A T ---			ATGCAGGATGAAGGTGGACAGGGAGG/ATGAGGGCCCAACCTGTCATCCAGGGCCTGCAGATGTCG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 149	G T ---			ATACTAGTACAAGTGGTAAATTTTGTACATTACACTAAATTTATTAGCATTTGTTTAGCATTAACCTAA TTTTTTCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAA TTTTTTTTCTCTG/TAAAGTGCCAGTATCCAGAGTTTGGTTTTTGAACGTAGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTTCTGTCTGGGGTTTTTGGTGCATGCA
ESTD- KRT10b	183 C T ---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACCTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAG/C/TGTCTTTTAAATAGT CTCTGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT10a	133 A G ---			CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACCTATTACTTCTA/A G)GAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTC TCTGCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT8b	231 C T ---			ACCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCCGTCTCAGGTTTACC/C/TGTCAACATTGACACA
ESTD- KRT8a	21 C T ---			ACCCTCACCCCTCCCTTAGCC/C/TGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCCTATCTCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
EST75099 6	82 C T ---			CACCTGTGTGTCTAGATCTCCTCAGTGGCCGCTCTACTGGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA/C/TGGGGGCAACCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGCCCCACC CCTCTCCTGGCCGCTTTGAGGTGGG

ESTD-LF79	142 A G ---	---	GGGTGATTTGAGGCTCAGTTAATATTCAAATTTAAACCGTAGCAAACTGCATTTGGTATTAGA AAATATAAAATTTCCAATATGTAGTGTGTATACCTGCTGCTGCCATGCAGCATCATAGCCTGT GGGAACC[G]GGAGGGCTTCCTTACCACCCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGACCCAGGCTTACCCCAATTAGGTGAACATGGCTTCGAG AGAGTTG[A]CAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCTGGATGA
ESTD-LMP2	35 C G ---	---	A TACACACTTTCCCTTACCCATTCACTGAAACGACT[C]G[G]CAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCTTAGGGGCACTCACCACCTCCAGCTTCTTCAGCTCTGCCCTGCTGCTGCCCTGCA AGGTTTGTCTTAATTCATCAATCAATGCTCTTCATCTTTAG[C]TACGCTGGGGTTTGTGTTG TTCTCTGTTTGTCTTAGTATCTGACTAGTCTTTAATTAATAAAGAGATGTATCTAAACAAATAG AGATTGTATCAGAAGTTCACAACATTTATAAAATTTTTCACCTG
ESTD-MCC	45 C T ---	---	TTGTCAGGAGTGTCTGATGCTGCTGCCCTCCAGCTCTGCTCCCTAG[C]T[G]GAACCTCAGGACAACGTGC AG
ESTD-METH	118 C T ---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCGAA TCTCAGGAAGTCTGTCTTCCAAAGGTTTGGTCAAGTTGCTGATTAC[C]TGGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGTTCTCTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAC[T]AACCAGATCCACAGACTGATATGGCTGGT AACATGGACTTGATATTTGTACAAAAAAGTTTATTTTCTAAAAAAGAAAAAGAGAAA AAATTTAAAGGGTGTACTTATATCCACACTGCACACTGCCTT[G]GCCCCAAACGCTTATTGTGT AGGATCAGCCCTCATTTGTGCTTTTGTGAACCTTTTGTAGGGACGAGAAAGATCATTTGAAATTCT GAGAAACTTCTTTTAAACCTCACCTTTGTGGGGTTTGTGGAGAGGTTATCA
ESTD-NFKB1	107 A G ---	---	TGTCCTAGGCCCCAGCCCTGCTTGTCTCCCTGGCTGTTATCTTC[A]G[GTACTGCAAGAGAACACA GACAT
ESTD-NPPA	45 A G ---	---	GTGTTTCTTAATCTTTTCCAGGAACACAGTGACCATATTTCTTCTGCAGGCATATAGAATTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGATACITTTTGTGATTATATATAGCAATTTGAGGG ACAAACCATAGTAGGCAGAAATGGCTTGAATAGTAGTCTTATTTAACCTTGGCAATAGCATTTG C/TATTCCTCTGGTTTATAATAAAAT
ESTD-NRAS	202 C T ---	---	GCCACCAACCCACCCACACCTCCACCTCAGCCAGACAAAGTTGTTGACACAGAGAGCCCC TCAGGGGCACAGAGAGAGCTGACACGCTGGGG[G]G[GT]CAGCCGTGATCATCGGAGGCGCCGGG CACATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCCAAGTCTCTAGACAGACAAAAC
ESTD-PA1	100 A G ---	---	TAGACAATCACGTGGCTGGCT

ESTD-PAR	120	A	---	---	CTCTTCAGGAACCAACAGTCTTACCAAAACACGACTTATTGCTGTCCGAGAGGTACAAACCCGTAGA
ESTD- Per/RDS	74	A	G	---	ACTTCTCCTAACTGTAATTTAGTTAAAGGAATCGAAACGCTGCTCTGAAGACATGGAGATACTGCCT
EST68308	5	29	C	T	--- AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTCTTTCACCTTCTTCTAGTGTCTAGAACGTTTTCTAG
EST54045	6	39	A	G	--- GACTGGCAGTTTAAGCTTTCACCTTAGGCTTCTGTATACCCATGCCC
ESTD-PXMP1	88	A	G	---	ACCTACAGACGTCGCTGGATGGTGTCTCCAAACCCGAGGAATCTGAGAGCGAGCAGGGCTGGCTG
ESTD-RDS	127	A	---	---	CTGGAGA/GGAGCGTGGCGGAGACCTGGAAGGCCT
ESTD- s14544	94	G	T	---	GGAAAGAGATTTAAGAAGCTTGATTTGGA/C/TAATCTGGTCTTTGAGTGTGGAAGAGTTTCATGTC
EST52908	0	45	A	C	--- TCTGCCCTGAGTTACAACAGATCCTTTAGTACAGCGAGTAATAGATATAATTCGACACAGATGGGAAT
EST19590	55	C	T	---	GGAGAAGTAGACTTTAAGGTAAAGTAAGAGTAGTTATTTTTTA
EST76136	39	C	T	---	GGAAATTTAAAAATATTTTAAAAATACCTCCATTTTGCTTGA/GTCCCTTTAGTGAAGATGATACCTGC
ESTD-SPTB	176	C	T	---	AAAAGACATGGCTAAAGTTATGATTTGTCATGTGGCAATTTTCTTACAAAATCGGATGGGAAA
					TCTGTTAAGTAAGTACTGTTTTGCTTGGCAATTTGATTTTAAATGTTGACTTTATCAT
					ATGAAACATGGTCTTTAATTTATGATATGTTTGTATAGCTATCTTAAAGGGCTTCTTTTTTTTA
					ATGCAGAAAGAGGGGAAAAA/G/GAGCGAGCTGTGGTGACAAAGGTGTTTTTCTCAAGGCTCATAC
					AGATTCGAAAATCATGGTCCCTAGAACATTTGTAAAGAGGTAAAGTCTTATGAAATTTATAATCTT
					CCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTGTGGAGAAAGCGTGGCCGGAGACCTGGAAGG
					CCTTTCTGGAGAGTGTGAAGAAGCTGGGCAAGGCCAACAGGTGGAGCCGAGGCGCAGACGCAGG
					CCAGGCCACAGAGGCTGAGGCGCTGGGCGCTGGGCGCTCCCTCCCGAACACTGAGAAATAGTGCAC
					CCAAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
					TTGGGAAGTTAGAGCCTATATTAATTTACGGAATTACTAAGCAGGACACAGAGGCTTAATTGAAAA
					TATCCCAAAGTTGAAATGCTCAGTTG/GTCTGTGTGGTTAGATGCAGGATTTATATGATCCGTTA
					ACCTCT
					ATCACAGGCTCTGGTCTCTGGCCATCATTTCCCTGGGAGAGATGG/C/CTGGTGGTCTGCAAGCCCTT
					TGGCAATGTGAGATTGATG
					AGGAGAAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGAGTGAAGATGT/C/TTGGCTCAG
					GATGCCGGAAAAATGAC
					TGAAGCTTCTGCCACGCTTGCAATGTTTCTAGGAGAACCC/C/TTGCGTCTATACCTTTATCTATAGCCCT
					CCCTAGGCTT
					TGAACACCTGTGGTCCGGAGCCAGGTGTGTTTCTCTCTGGAGCCCTGAGGAGTTTGTGTGTGTG
					CAGTCCCCCGGCCACCTGCTGGTGGCCCTGGACATACACCTTCACTCCCTTTGGCCCGGAGAGAC
					ATTTACCACTGGCCATGTCCCTGGCCCTGTTGTGCACA/C/TTCTCTGTGAAGACCCCAACCCCTGC
					CTCCCCACCCAAAGCCAGTTTCTAGCAAGGGCAGGAC

ESTD-TAT	224 C ---	---	---	AAATGGTCAGGACCCTGATCCACAAGAGTGATGTAACATTCATCAGGGCCATCAGTTCAITTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCAATCATCTTAAATGACTTGTGGACAGGATCA ATTCCTCTCACCTAGAACGTTTGTACAACTTTCTCCAGATGGAATGGGATATGATGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THRb	125 A C ---	---	---	TGGGCTTTCTCCGGCAGGTAGACTTCTTACTTGGCTGTGATTTCCAAAGAGAAAGAGTCCCAAG CACAGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAAATCACAGGATC(A/C)CTTCAT CCACACTGGATTGGCCAAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCCTGTGAGCTTCTGGATTCTTGTCCCAACCAAGAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGCTCTCCAGATTTCAGTATCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCATAAATATTGATGTCGTTAAA CATGGGTGTGATCCATTTTCAATTTGGCCATAGGTCCTATGGGGATGACA
ESTD-TYR	122 GT ---	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCOCTACTCTTATGCAATAGTATCACAA AACCACCTGGTGAATATAATAGATTGAGTTAATACTGTATTTCTTCACTTTATTACCTTCTTCT AATACAAGCATATGTTAG(A/C)ATTAAAGTTCTAGGCATACIT
ESTD- TYRP1	222 A C ---	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTTATGCAATAGTATCACAA AACCACCTGGTGAATATAATAGATTGAGTTAATACTGTATTTCTTCACTTTATTACCTTCTTCT AATACAAGCATATGTTAG(A/C)ATTAAAGTTCTAGGCATACIT
ESTD- VB12	148 C T ---	---	---	TCCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTCACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA(C/T)CAGACTGAGAACCCAGTATATGTACTGGTATCGACAAGACCCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T ---	---	---	TCCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACAC(A/G)TGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTCACAGAGACAGGAACACCA GTGACTCTGAGATGTCAACCCAGACTGAGAACCCAGTATATGTACTGGTATCGACAAGACCCCGGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G ---	---	---	ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAAGCCAGTCCTCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCACTGGAGAACAAAGACAGCCACAGTGGCGCGGGATGGCGGGGAGTTCC TGTTGCGGCCACGGCTGGCTCGTTGTGAACGGTAGCCTTTCGGTTGCGATGCCTAAACCTTTGT TTCTTGGCCAAAGGAGGGGGTGGCCATGCCTGAGATGTAGATGGGCGC
ESTD-VWF	36 G ---	---	AGGTAGGAAAAGCAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCTTTGG TCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACCACTCTCAGCTCAAGCCTCAGCACCCAGATGCTGTTCTATAAGGATGACGTGCTTTTACAA CATCTCTCCATGAAGAGCACAGAGAGTTATTTTCTCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAAACCACTGCAGAGTACCAGTC/GTGTGGTGGGA AGGAGTGGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAAGG
ESTD- TNFAb	152 A G ---	---	TTCTGTCATCTGTCTGGAAGTTAGAAGGAACAGACACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGAAGGGCATGAGGACGGGTTTCAAGCTCCAGGCTCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCTC/GAATCGGAGCAGGAGGATGGGAGTGTGAGGGTATCCTTGTGATG CTTGTGTGCCCAACTTCCAAATCCCCGCCCGCGATGG
ESTD- TNFAa	88 A ---	---	TTCTGTCATCTGTCTGGAAGTTAGAAGGAACAGACACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTGAAGGGCATGAGGACGGGTTTCAAGCTCCAGGCTCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCTCAGAAATCGGAGCAGGAGGATGGGAGTGTGAGGGTATCCTTGTGATG GTGTGTCCCCAACTTCCAAATCCCCGCCCGCGATGG
EST52418 6	113 A G ---	---	CAAAATACAGGGTCAACTGCTATGATGTGTTGGAGCCCCAGTCACCTTTGGTGGCTACAAGATGCG GGGAGTGGCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACT/GAAGTGAAAACCTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACCTCTATTTGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC/GGAGGCTGGCTTATCAGCCTCCAGCCAGACCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCCTGCC CCGGTCACTC
EST51976 7	123 A T ---	---	AGGCAGAAACTGGCCCCCATCGGGGGACGTGGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAGGTCAACTCCTCTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAG/ATCTCTCTC CCTCCCTGAGCTGGAGCAACAGCAAGAAACAGCAGCAGGAGCAGCAGGAGGAGGTGCAGATGCTG GCCCCCTTGGAGAGCTGAGCTGCCCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCATCTTGTTCGAGTTT CTCTGCCATGTTGCTATTGACGACGGACCTGTCCCAGCCAGATGATTTACCATTTTCCACAGTGGT CCC/GTAAAAACAATCTATGAGCCAGGAGAGAGATTACGTATTCTCTGCAAGCGGGGCTATGTG TCCCAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60 C T ---	---	AGACCTCAGTTTCCTCTCTGTAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGC[C/T]AGCA CTGGTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGGACAGGTGGAGAGGAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAGAGCTGGGAAATGTGG
EST39852 8	106 C G ---	---	CGGCTTCCTCCAGGTATTGTCAGAAAGCCGAGATACCTCTATGTCTCAGATGCATTCCTAAG GCATTTCTTGAGGTGAGTACACCTTCCCACCTCTT[C/G]GGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTGGAAAGGCCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ---	---	ACCTGGGTGTTGCTGGTGCTGTGGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCTGGGGCCGTGG TCTCTCTGGTGTGCTGGGTAGTCTTGAGTCAACGGTGTCTCTT[AG/G]TGAAGCTGGTGTGATGGCA ACCTGGGAACGATGGTCCCGAGGTGCGGATGGTCAACCCGGACACAAAGGAGAGCGGTTACCC TGGCAATAT
EST38027 2	120 A C ---	---	AGTGACTCCAAGGAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCACCTGCAAGAACAGCATTCATACATGGATGAGGAGACTGG[A/C]AACCTGAAAA AGGCTGTCATCTACAGGGCTTAATGATGTTGAACCTTGTCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTTGATAGTGGCTGCTCTAAAAGACAAATGAATGGGAAAGACAA
ESTD- COL2A1cc	112 A G ---	---	AGAATGTATATAGTCTCAACTGGCCATCTCCATTTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTTATGCTCTCTTCTGTCACCTT[C/G]GGGTGTTCAAGGTGGAAAA GGTGAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCT TTGTCAGCCTATTGAGCTGTAATCACCATACCGTACCT
ESTD- COL2A1dd	97 C T ---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGGACCTGGAACA[C/T]TGGACTTCTTCTACTGCAAGCAGACAAAGACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAATTTTATTTGACCACAACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ---	---	GCCGAATGCCGGGAGTTTCTCCAATGTGTGGAGAAGCCCTTAGAAGACATGTTTGATGCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCCTCTCATCATGAAAAAC TGGGAGCCCGGCAT[A/G]GTGCTCATGCCTGTATCCAGCATTTTGAGAGGCTGAGCGGGTGGAT CACTTGAGGTCAGGAGTTGAGACCAACCTGGCCAACAT
EST12274 0	135 A G ---	---	CCCCAGTTGACAGCCACTGCTAGACTAAGTTCTTGCTTCCAAATAGAGCCCTTACCAAAGTGAT TACATAAAGAAGTCAAGTGGTTTACTCTCTCATGACCAAAATATCTTCCCTCCTTAGGATGAGGTG[A/G]TAGTAAATGACCGATGGGGTCAGAACTGTTCTGTCCACCATGGAGGATATACTAATGTGAAGA TAAATCAAGCCACAGAGCTTGCCAGATC
EST76807	91 G ---	---	ATGCTAAGGGGATCGGACATGAAAGGACCTGTGAGCCGATTGTCTATCTCCAGGGCCCTGTCTATC CAGCTCACTCATCAATGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCACCACTGCCCCCT GCTGCCATGTGGACTGGTGTCAAGTTGAGGACTTCTTG

ESTD-SSA1	111 C T ---	---	---	TTACATTTGTGGATTGTTCTTTTGTGTCAGCACCTTTTCAACATGATGTATGCCCATTTGTCCAAG TTTGCTTTGGCTGCCGTGCTTGTGGGATATTTGAAAGAGATC/TJTTGCCAGTCCAAATGTCTCTAGA GAGTTTTCCCAATGTTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTTAGATTTAAGTCTTTAATCCATT TTGATTGATTCTGTA
ESTD-RYR1	109 A G ---	---	---	CTTCGTACGGGAGGTCACGTCCTCCGCTCTTTCATGGACATATGGATGAGTGTCTGACCAATTTCCC CTGCTGACAGTGATGACACGCGAGACTTGTCTACTATAG/A/GJGGGAGCTGTGTGCACTCATGCC CGCTCCCTCTGGAGGCTGGAGCACTGAGAAATCAGCTGGAGTGGAGGCCACCTGGCGTGGGGCCAGCC ACTCCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-WT1	70 A G ---	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCCCTTACTCTCTGCTGCGCTGCAGGATGTG CG/A/GJCGTGTGCTGGAGTAGCCCGGACTCTTGTACGGTGGCATCTGAGACCAGTGAGAAACGCC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-F2 EST44438 7	100 C ---	---	---	GATAAGTACACTGAGGCCCGGAGGTTATTGCCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAAAGGCCGTAGGGGAACTGGGGGATCTAGGGGATGGGTGAGGAATGGCCC AGCCAGTCCCGGCGGTGCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGGACAGGAGATGGGC TGGATGAG
ESTD-PBDA	103 A G ---	---	---	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGA/C/TJG TCCTGCTCCGACCTAAGGGAGAGCCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	122 A G ---	---	---	CCTTCATGCCCAGATGGAATTCAGTCCCTTCCAGTCTGCTTACCTGACAGTCTAACCTGTACAGTCTAAAGAGT CTGAGCCGTGGTGGGAAGGCGAGGACTAATCCAAJG/TCTCTACCCGCGAGCTTGTCTCGCATACAG ACGGACAGTGTGGTGCAACATTGAAAGCCTCGTACC
ESTD-CTLA-4	48 A G ---	---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAG/A/GJTCAGTCCA AGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACCTTGAATGTATTCAAC TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
ESTD-ACE	96 C T ---	---	---	ATGGCTTGCCTTGGATTTCAGGGCACAGGCTCAGCTGAACCTGGCTJAGJCCAGGACCTGGCCCTG CACTCTCTGTTTTTCTCTTCTATCCCTGCTCTGCAAGCAATGCAAGTGGCCAGCCTGCTGT GGTACTGGCCAGCAGCGGAGGATGCCAGCTTTGTGTGTGATGTCATCTCCAGGCAAGCCAC GATCAAGCAGTGCACACGGGTACGATGGACAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC/C/TJGTCTCCCTGGTGGGGGCCAACCCCGGCTTCCA TGAGGCCATTGGGACGTGCTGGCGCTCTCGGTCTCCACTCTCTGAACATCTGCACAAATCGGCCTGC
EST54419 8	88 A G ---	---	---	CTTCTGCCTAATTGAATGATATTGTGCTGTGGGACCTGAGCACCTTTTATGGCACAATGATCACTA TTTTCTTGACCCCTACTTACJAGJATCCTGGGAGATGATTTGGGTTAGCGTGGTCTGATGTTGCTA CTATAGTCCAAAGTGAA

ESTD-PS-1	99 A G ---	---	GGGGAGTAAACTTGGATTGGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACCAATAGCCTAGTTCGTAGCCATATAATTTGGTTTGTGCCCTTAC ATTATTACTCCTTGCCATTTCAAGAAAGCATTGCCAGCTCTCCAAATCTCCATCACCCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	GGCTGCCAGGGTTCCGTGGAGGGGCGCTAGCCGGGCGCTGCTGGCGTGGCGGTGCTGGCCACC GTGGAGGCAACCTGCTGGTGCATCGTGGCCATCGCCCTGAGGCTCTCTCCAAATCCATTTCTCAAAG CGTTCGTGACTTCGCTGGCGCGCAGCCGACCTGGTGATGGGACTCCTGGTGTGCCGCCGCGGGGCCA CCTTGGCGC
WI-567b	48 A G ---	---	TCTCACACTGACCCCTTACCTTCATCCTCACCTCTGCTGCCCTTGGTTC/GJAGCCCTCATCTCTTTA CAGGATCCGCCACAGCATCCCAACTGATCTGGCCTTAGGCTCTCTCCAAATCCATTTCTCAAAG GCTGCCACTGTGATCTCCCAAAGGTGATCTGATGCTACCATCTTGCITCAAGCC
WI-801c	58 G T ---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTG/JIAGATGG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCCACCAGAGAGTTAA CATTTCTGCCACCCCTC
WI-801b	58 G T ---	---	ATGGAACATTTCTCCATAATGAATGAGGTCTCAATCCATTACACATCCCTTTCTG/JIAGATGG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTGCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCCCACCAGAGAGTTAA CATTTCTGCCACCCCTC
WI-1099b	76 A G ---	---	GAAATTCACCTATACAAGAACTATTTCTCTAATTTACATTAGTCTCATTATCTGAAATATTAT TTTTTACA/JGTTACCCCTTTGATTTTGTGATTCATTTGTAACGAGAGATTACAATATCAGTAACGC TGTTTCATTGATAGTGCTATCACAATGTCTAAATACITTTTGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTTGCTTTATGGTTTA
WI-2529	71 C T ---	---	AGGAAATGGCTGATACCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTTGATGAGCCTCT CAA/C/TCTTAAGTCTGCTGCCCTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGAGTAAAGAGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTTTCATTAGAAATGGCTTTGGGATGACAAGTA
WI-10088	205 C G ---	---	TAAGGGCTGTCTTCCCCAGAGGGCCCCACGGACAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGAGACCTGTACCCCTATGAGGTAACTGAGGATGAAGGA GTGAGTCAATATTGGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAGAGACTTTTACATTTTAGAC AGG/C/GJAGCAGAAGCAGCAAGGAGAAAGGAAGT

WI-2015b	190 A G ---			TGTCAGATAGTCCGCTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCT ATATATTTATACAATATACAATTACTTGCAGATAGCATGACATGCTAGTGAACCCACACAGACTAT GTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACATGGTGTCTTTTCCAACT[AG]CATATACTT CTAATACCATAGAG
WI-754b	49 C T ---			GAAGGCACAGGGAGAAGATGGCTGTCATCTACCCAGGAGAGAGAAAGC[C]TACATTTATTGGTAA TCCTATAAAGTGCATCTTTAAATTTGTATTACITTAGA
WI-754	22 T C ---			GAAGGCACAGGGAGAAGATGGCT[C]GTCTATCTACCCAGGAGAGAGAAAGC[C]TACATTTATTGGTAA TCCTATAAAGTGCATCTTTAAATTTGTATTACITTAGA
WIR-1b	56 A G ---			AGGCAATCAGACCTACAGAGGAAACCCCAATAAAACTCTGATGATCGTACATCC[AG]TGGCGTG GAGGGTGTGCTCTCTGAGGACATGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-1	56 A G ---			AGGCAATCAGACCTACAGAGGAAACCCCAATAAAACTCTGATGATCGTACATCC[AG]TGGCGTG GAGGGTGTGCTCTCTGAGGACATGGAGCTTCATGTTTGGAGCCCTCCCTG
WIR-3b	72 A G ---			TAATTTAAATGGGGCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT[AG]TCTAAAGTTATTAGCTCAGAGCCTCACACATCTCAGTACTGATAAACAATAAGCA AAGCTGGTGTGAGATAAGA
WIR-3a	69 A T ---			TAATTTAAATGGGGCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GA/ATGTATCTAAAGTTATTAGCTCAGAGCCTCACACATCTCAGTACTGATAAACAATAAGCA AAGCTGGTGTGAGATAAGA
WIR-4	47 T ---			GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATCCCTGCTCACACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGCC
WIR-5g	209 C ---			CGGGACAGAGACAGACAGAGAGAGTCTGCGAGATTCAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5f	196 C ---			CGGGACAGAGACAGACAGAGAGTCTGCGAGATTCAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5e	194 C ---			CGGGACAGAGACAGACAGAGAGTCTGCGAGATTCAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTACAAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGCTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5c	177 C	---	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGCTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTTACGTCCAG
WIR-5b	159 A	---	---	---	CGGGACAGAGACAGAGAGAGTTCTGCAGCATTACAAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCAGCTGTT AGGTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACAC AGGTTTACGTCCAG
WIR-5a	37 A	G	---	---	TAACCCCTGAAACCTTTGCTTCTCCTCATCTCAGGGAGAACACAGACTTTCATGTTAAGACCAGAA[VC] CGAGCTCTGGGGTGGGCAG
WIR-6	63 A	C	---	---	TTCTGACTATT[C]/AAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-7	12 C	T	---	---	GGCGTCTCTATGACTATCCTGGTCAATTGATTGACTAATGATTCCTG[C]/GGCCCTTG
WIR-8	46 C	T	---	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACATAAAGTTGTCAGAGAGGATGA[C/G]CTGAAG AAAGAACTTACTCTCTTTTGACCAATAAATACAAATTGGGAAACACTGGAAACCATGGCTTGATTACT GACAAAC
WIR-2	56 C	G	---	---	TGTCCTTGCTTATGCCTGCTCTTCGCTTGGCAGGATGCTGTCATTAGTATTTACAAGAAGTA GCTTCAGAGGGTAACCTTAACAGAGT[G]/A/CAGATCTATCTTGTCATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTACTGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACCCTGTTCTCACTC
WI-7069	93 G	A	---	---	GGTCATTTCCTTTTATCTGTGTCAGGCAGCCAGCTGACTTTA/TCTCTCTGTTCTGTCATCTCCCC CCACATACCAACTTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18694	41 A	T	---	---	CACACTGTTACACACCTATATTTCAAGTTTGGAAATGC[A/G]TATTTGCAAGCAGCAATACAAAAGTA TTCATGAAGAATGCATAATCTCTGAAAAATTATGAAAAACATCCCT
WI-18612	37 A	G	TGC	CTTGCAAAAT	TTGATTGCTG CTTGCAAAAT

WI-18517	87	C	T	CAGCCTGA	CAGGAATCAG	TGTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCCTCAACACCCCCCTCCATTTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA[C/T]GTGTCACCTTGTCACCAACACAACTGACTGC
WI-18668	76	C	T	TAGGCAAAA GC	GGCGAAAAAC CTGCACTTTT	GCTAAATTAAA CTGCACTTTT	CGATTGACAACCTTTTATTTTCAACTTAGGTACAGTCCAAATCAGTGTAGATTGGCGAAAAACT AGGCAAAA[C/T]AGCAAAAAGTGCAGTTTAAATTAGCAAAAGGCTCAAGACAGTATGTGGAAGGAA GGTGAGATTCCCTCCTACT
WI-18680	75	T	C	A	AGCATCTGGA	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGAAGCATGCATCCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT[C/G]CTCCGTTGTATATTCAGGAGGGGA
WI-18704	99	A	C	GGGTAC	GGGTCTCCGA	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTCTTGTGCGAGCACCACACCAAGGGGAGGTTGGGCTTGAAGGAGCC CTTGAGGAACACGGGTTCTCCGAGGGGTAC[C/G]CCAGCAGGGGCTTCAGCTTAAAGTCG
WI-18673	29	A	G	---	---	---	TGTGGCAACCTTGTTTTAAATTGCAAA[C/G]ACTTAAATTTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAAACATATGAATATATAAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAAGCGCATACAAGGAAG
WI-18640	121	T	C	GGG	GTGTTGGGTTG	GCAATACCAC TGAAGAGGAC	ACCATGTCATGTTTATTTGGAGGTTAAATCCTATTAGGATATGAAAGGATTCAGCAACGATTGAGATT GTGTTCTCACGGAGGGCTCGGGCCAAAGTCTGTGGGTGGGGGTGCAGAT[C/G]GTGTCCTCTTC AGTGGTATTGGGAC
WI-18533b	91	T	C	---	---	---	GGGAGAGGAGGTAGATTGCCAAATGAGGCATTTTAACTCCCGAGATTTCCTTTTATTT TATATTTTCACTTTTTCATCCTAA[C/T]TACTGAAGCCATTTCTTTGGTTAACTTTAGA
WI-18533a	59	T	G	---	---	---	GGGAGAGGAGGTAGATTGCCAAATGAGGCATTTTAACTCCCGAGATTTC[C/T]GCTTTA TTTTATTTTCACTTTTTCATCCTAAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83	A	C	TTC	TCATCTGATAC CTTGTTCAGAT	AACGAGATA AGGTACAACT	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTTCATCTGATA CCTGTTCAGATTTC[C/A]AAATAGTTGTAGCCTTATCCTGGTTTACAGATGTGAACTTT
D49493	159	A	T	TCTGGGAATT	CCTGAAGGAA	ACTTTCAGGCC AGGGC	CAGGACTTGTGGTGCAGCTGCAGACACAGACAGCAGCTCATGGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATTAGGGGGTCTTTCATTGTAGTACTAGGCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAAT[C/A]TGGCCCTGGCCTGAAAGTGGCCCATCATTCATACCCACTGTT CT
EST10030	98	T	C	TCTCAAGTCCC	GCAGTGGTGGT	ATGGATGA	TATTTATAGAGGAGACCTAGGAGGAGTTGACACAGCACACTGCTCAGCAGATGACTTAAAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCCT[C/T]CATCCATACCACCAGTGTGATTG
EST10052	24	G	A	GAGGCTG	GCTCACTTCTG	TGTGGAACCTC AATCTTAGACT	TATTTGGCTCACTTCTGGAGGCTG[C/A]GAAGTCTAAGATTGAGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTCAATAACCTGGTGGGAAGTCATCATGTGGCAAGAGAGAGGGCTACAGAGCAAGAGGAA A

EST10605 2	118 C G ---				CTTGCCTAAATCACAGTTCTGTATTATACAAAAACITTTGTTTTCTCTGACAAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAAATTTGTGGAGATGCCCATGT[C/G]TTGTGAGACTTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G ---	CTCTCAAGTAG ATAAGAGGCA TAATCT			CATGTGTCATCCCATGATTGAAAAGACATGTGCTCTCAAGTAGATAAGAGGCATAATCTT[G/J]AA ACAAAATCTTTCTGAAAATTTAGCTTATGAACCTCATACACTGCAACCCAGAGAGGAGGCAC TATGAGGCCAGAGGAAGTGACACTATATGTGGAAGTCTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11260 8	101 G T ---				TTTGATGGAGAAATCCGAGGCTGCCAGCATCCCAAGTAGATTTCTTTGGACGAAGAAAAATCCT TCTGTGGATTGAGCTTTACCGCTTTCTCTCATCTGCTGGT[C/T]TTCTCAGAGCTTTAATGTCCGT CCTGCTCTCOGAGTCAG
EST11349 9	109 C T ---				GAATCTGGGTATTAATAGCGGTGCCACAGGAGCACATAGGAAGAGCATCCAACCTACTTTGGAG CCCT[G/J]AGGAGTTTTAGAGAAAGCTGGAGCCGGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGAGGAAGGAGTGGAA
WI- 16632a	71 A G ---	CCAACCTACTTT TGGAGCOCT			CCAGGAATAAAGAAAAAGAGTCAGAGGAACAGCTTTTGATGTTATGAGGCTGAGACACTACTC TTCCCTCA[G/J]GACTATTTCTGACTATAAGTGAATAAATACATTGAAGACTTTCAGGAGCTCA CTTGCCATTTATTTTGTGCATGTGTTCTTAAAGGCTTGAAAGATAAATTTGGAATGTGGGAAC ACATAGATCCCAGA[G/A]TTTAAAGGGCTGGAAAAAGTAGCCTTAAGAC
EST11772 6	74 A G ---				AGAGCAATGGTGGATCTCAATAAGCAGCTCATTTTGATTAC[G/A]GGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAAAGCTCCACAGAACTTTTCATGCACCCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST11795 3	82 G A ---	CAATAAGCAG CTCATTTTGAT TAC			GOCTAGTAATTCCTAAAAGGAACATGTTTGATATAAACACTCAGTACAAAAGTCTGT[G/J]ATCCAGG AAGTGACCAGCCCGACGTTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAATC GTGGAAAAATTTTTATCTGTACGCTCTTCC[T/C]ATTATATTTATCTTGCTCTTGATTTCAGCACCC CACCGATTTCAGGCAGTGCTTTCTAAACTGTGCCCTGTGAGCTGTTAAAAAGTCTCT
WI-16644	42 G A TAC				CCCTAGCAATGACTTGGAGTTGTGTCCTCAATACCAAGTTACATACTGTGGCAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[G/J]GGAAACGCACAGCAAAATTGACGATGCAGCTTTTAA CCTTTTTA
EST12005 9	56 A G CAAAGTCTGT				ATCTTGAGGTTTCTGGGCTGTGAG[G/J]AAGTGACATCTTTTACTTACCACAGGTGAGGAACCCCTAT AAAGAACTGTGTAGAAAAGATATCAGGTGAGACTTTTTTAAAGGGCTTCTTATCAGCTCAATAAA
EST12055 9	32 T C ---				
EST12492 1b	95 A G ---				
EST12492 4	25 A G ---				

EST12502 2	52 C G ---			ATACTAGGGAGAAAAACCAACTGGAGGGAAGTCCACAGGTCACACTTGTCA[C/G]CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAAATGCTACGGGGGAAATGAOCCATTTTAAAGGGCCATGTG GTCGTCGAGGCAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATTAGAATGTATCGGTAAAAAGAAATAGGAATGCATATTTCAACTCACTGTCAACAA CAGGTGTTTTATTATCCCAAATGACAGTGTTCCTGAGATTC/GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCTTCATTATTCATTGTTCAAAACACACTGTCTAGTACCAACATTTGCCACCGGC[A /G]TTGAGAATACAATATTGAAGAAGAGICACTGCCCTGCTGGAAAAATCAGAGTATTTGA
EST12817 9a	22 C A ---			TTGGGTTCTCCAGGATCCAGIC/AJCTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGG GTTCITGGGAGTGACCGGGATGGGAATCCATGTTCCTTTCGCTACTCCATCAGGTCAATGGC
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA/T/AICAAACAGCCAGTATTTACCAGAAATTTGTTTGGGTTTCA ATGTAGTGTTCAGCTTTAATACACTGCACCTTGTITIG
EST12949 2a	52 A G A T A C T G T T	GGCTTTAATCA TAACCTAATA	TGTTGCTCTGT GGGTCTC	AGGATTTTCATGAGGCTTTAATCAACCTAATAATACTGTTAAAAACAACAC[A/G]TCTGTCACTTG CAGAGACCCACAGGGACACACATTCCTCTCTCATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTTTGTGTTTCTTAATGAAGCATAATAACAGTTAAAACTCTCAGAAAAATCATCTATAGTTGA GTGTAAAACTCCCTAAATCAGTCTTCTAGGGCCACA[C/T]GGAGCAGAAAGCAGCTTCCCACCCCAAG CACTCTGAACT
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCTTTTAAAAATTTAATCGCTTTATACAATTGACACCAAAATAAATGCAC[A /G]TATTTAAAGTTTACAATTTGAGAAGCTGACACGTGTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCGTCTTTAAAGATTCCTTCATAGCTGCTTAGGTTTGTCTTCC[C/T]AGCATAATTCAGCTATAATCA CCTAGATTCCTCCACAAATATTCCTGTGTGTGCCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGCTTATTTCCACTCT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTTGAGGAAATAAATTAATGAAATAGTCT GGCCATT[T/G]GACTAACAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAACATG
EST13230 6	72 G A	GCTCAGATGTG AGAGACGC	CCGGCTCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTACAACCAACTGCCGCTCAATATGCAGCTCAGATGTGAGAG ACG[C/G]ATCTCTGTACAGGCGGCTACTGTCTTCAATCCTTTGCAATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C T C T C A G G C C T	AACAGAGGGTT TGACAAAAGA	G	AAAGATATAAAACAACCTCCCATCAGTAGGAATACAAGGTTATACATTTTAAACCAGATTTTCTCAGG CCTT[C/T]TTTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAAACCCCTCTGTATATAACCA

EST13278 2a	51 A G	CITTCACCGAA CAATATTTTAG G	CATATCTTGG GTGGTGAGAA	TTGCGAGAACGTTTACAAGCTCCAAACCTTTACCCGAACAATATTTTAGG[A/G]ATTTGAAATTAT TTCTGTAGTTCTCACCACCCCAAGAAATATGACAGCTTG
EST13282 0	99 A T	CCACACATTTC AGTCCAAAGA	GATGGAAAATT TGAGGAAGGTT	GCTCACTAGATGAGCATTGACCAAAATATTTAGATAATACCTGTGGGAAAGTGCTGAATTACTAGCC TGCCTGAGAATCCACACATTTTCAGTCCAAAG[A/T]AACCTTCCTCAAATTTTCCATCTCCCATCAGA GG
EST13290 9		CAATTTTITAGA AGTTGGGTTT	AAATCACITTC TGGAATTTCA	AGCTCATCTGCAAGCAATTTTITAGAAAGTTTGGGTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACITTCAGTTACTTAAAGACCTAAAGACAAAGTGGTATCACATCACATATTTTGT ATGTGGGGCTTTTITG
EST13518 2	39 A G CTT			GAAACATCCTCCAGTAGTATTGAGGTTAAATGATTCAGCATT[A/C]GACTTTAAAAATTACCTCA ATGTTCTCGGAGTCGTCATAGTTTAAATGACTTCTGCACCTTCCTTATAACCTTGATTG
EST13522 8a	45 C G			CAGGTTGGTATTCTCAACTAGGAGCTATTTTGGCCCCCATCCCCCGGCGAGTGCTGGAGAC[A/ G]GTTTATTGTCACAACCTGCGAGAGGTGGGTGCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	66 A G			CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGGCCATTGGTCTAGGAGTAGA AA[T/C]GCACACAAGGAATAAGGAGAGGAGGTTGGTGTAGTTGAGGGAGAGAAAGTTGGGAAGCA TTTCAAGCTAAGTAAATGGT
EST13785 0	69 T C			AAGATTACGGACCATAAGAACTGCCCCCGACCCATACACACACAATTTATAGCAGGTAACCA CTGAAAGGAACAAAGTAATGACTTCTTGAACAA[C/G]TGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	101 C G			CCTCAACCATCTGTAACCCGAGCC[C/G]CAGTGACCGGGACTTGCTGCTTCCCCATCCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	25 A G			CAATGGTGTCATGTGAACATAT[A/G]ACCTATTATCAAAAGTTAAAAATATCCCTTCTTGCAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGACCGAACAGGAGGGTAGGAGG
EST14221 5	23 A G			AAATCAATGCATCTTGTGGCATGCTAGACAGAGGCATT[A/T]C]TTTTGAAGATCTTTTAAAAAT ATTTTGACTGTTCCCCCTCACACTCATTTTAAATTGT
EST14812 2	42 T C	GCATGCTAGA CAGAGGCATT	AAAATATTTT AAAAA	TTCACTTAGTACCAAGGATGCCCTTCAAGTCAGCTTCTACATCTGAAAT[A/G]AGTACATAATGGG ATTTAAGTAAATCTTTAGAAGTCCCGGAGTTTGCCTTTTCTAACATTTTCATATCAGGTGAAAAACAAT TTTTTCATATGGGTGATT
EST14815 3	50 A G ATA		TATGTACT	TTTGCTCGGCAATACATAGTGGCAATGCGCGTGGAGTTCGGCCGCTCTCCCACTGAACCCAGTAAT TCACCAGACAATGGCGCAACCACTTAAATAAATGCGCGTCAATACCCCACTACTGGTT[A/T]TTCC GGTACTGTTTTCCCGTA
	128 A T	CATACCCACC ATACTGGTT	CGGGAACAA GTACCGGAA	

EST15420 6	109 C A ---			---	TTTAAACCCCAAGACCTTGATGTGACGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTTGTCATCATATAATCATATAGCCAAGGACT[C/A]GGAATTTTGGCTGCTTCAAGTCA TTCCAAACCTCTCTCAGG
EST15700 6	48 G C GGA			GGATAGCTGA AACAGAGATA TTATTCTC	GTCACCAGCACTTTTATTAAAGACGTGAAGAGACAAAGACAAACAGAGGA[G/C]AGCAGAGAAATAA TCTCTGTTTCAGCTATCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTAGTA
WI-16739	57 G A CACAAGC			GATAGTTGATG TTCATTATTCC CTATAA	AAGGATTGAAACATACCTAGATCATATAAAATTTGTGAAGGTTTTGCCATCACAAGC[G/A]TTATAG GGAATAATGAACATCAACTATCCTACAGCTAAACCTAATGAAGACCAAAATGGCTCCCAAGGT
WI-16782	96 C T CACTGTAAGG TC			CTTCTATCTTT CTGTTCTCTCA TC	CTTCTCTCTCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAAGG[C/T]GATGGAGGAACAGAAAGATAGAAGAGTTTGGGGT GCTGATGAAATTTGGGGG
WI-16783	64 A G G			TCCTGAGATGT CTTTACCTGA G	AAAAATGTAAACCTTAGAGGTTGCCCTCTTTGTGTCACTTTTCTCTGAGATGTCTTTTACCTGAG[A/G] CTAATAAGGATTGAACCAAGCAGTATTTTAAATGGCAAAAGTCCAGATGTAACCTCGAGT
EST15948 2	58 T C ---			---	CAGGACTTAAGTCAATTTTGCCTGGAAGACTTTAACTAAAGGTGAGGGCAACATAGGA[T/C]TGTGA CAGCACCACTCGGACCAGGAAGTGTGAAATCGTCACACTAGCGTGCCAGCCCTTTTTCCTGGC TGCTCTGCCTCCAGAGC
EST16088 8	89 G C ---			---	GGTTTGAAGACGCACTTTATCTCCACCTGCCACTGGGATCTCATTTTGAAGAGCTGTTTGTGAGCC TTTTCCAGAAAGGCCGCT[C/G]GGGTTTCTGAACCTCTATGGGCATTTTAGAAT
EST16089 9	96 C T ---			---	CGTCTGAAGTTTCTTTATCACAAGTCACATCAATCCCTCGGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCT[C/T]AAGAGGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G ---			---	ATCCAGCTGTGAAGGACAGGAG[C/G]GTAAACACAGTCCATTATAAGGGGTGTGCACATTCCCA GGGGCTCCAATAATGCAACATTGTTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTTGGCTC
EST16104 9a	83 A G ---			---	TTCTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAGTGATTTGCAG CTGGTTCTCTCCAGGGA[G/TTTGGCCCCGAAGCTGGCTCAGTTACCTCCAGGACCTCAGTC
EST16118 0b	119 T C ---			---	ATGGTATAACAAAATCAGTTCCAGGTTTTTTTCTGAACAAATGATCCTTTGGTCTTTCCCGTGGCATG CTCCTAAAACAACAACTAAACAACCCCTCTACGCTAATCAGTCACCTAAGATA[T/C]CGAGTGGCAAAGT CTTTCACA
EST16118 0a	32 C G ---			---	ATGGTATAACAAAATCAGTTCCAGGTTTTTTT[C/G]TGAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCCTAAAACAACAACTAAACAACCCCTCTACGCTAATCAGTCACCTAAGATATCGAGTGGCAAAGT CTTTCACA

EST16151 2	53 C T ---			AGCCAAATTCAAACGAACTCTATCAAAACACACAAAGGCCTAGAGGAGATTAT[C]TAAATGAACGT AAATAATTCAGGCAATTTTGATCTAAAGCATTTTGCTTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTTGATAGGA
EST16182 6	54 G A ---			CATTGGTTGGGTAGGGAAGATAGTAGTGTCAAAATAAAATGGTAAACAGCAG[G/A]AAATGGAA TTATAGCTTCTTTTCATATAGGGAATTGAAATTTATTTACTGAGGGTGATAGGCAGAAAGTAGTA
EST16183 2b	59 A G ---			GCAGGTAAACTGTGGTTCACACAGTATTGTTCTTTCTATAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACGTGCTTCCTGGCCCTTCTTCGTTTCATATTTTATGTCACTGTCTAAGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ---			AATCTTAGGCTCTTGGCTTTCAAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTGCGCATTT CCCCAGAGGAAAGATCAGCATCATAAACACATGGGTACATGCTCAGCAGCATGGTGTGTC
EST16229 2c	52 T C ---			TGTGAACCTCGAATTCGTTGTCCAAAGTCTGAGTCACAGTTTCATTTGGGAGT[C]CCCTGTGCAGCC CTTGCCAGTTCCACGAGGCAGGATACCTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
EST16229 2b	45 T C ---			TGTGAACCTCGAATTCGTTGTCCAAAGTCTGAGTCACAGTTTCATTTGGGAGT[C]CCCTGTGCAGCC CTTGCCAGTTCCACGAGGCAGGATACCTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
WI-16816	124 A G TGGGTTA	GGAGCCATTGT	GCCTAGATTTT GTTGAGGACAG	CAGACTTTTCTCAGACCTCATTGGCTGGAAGTGGTACATGCACATCCTTGAACATCATTTGGCAA AGGGAATGGTGCATCAAAATTTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGGTTA[G/A]GACTGTCC TGAACAAATCTAGGCTC
EST16269 5b	49 G A ---			GCCACTCTCCTGTGGCTTGTCTCCTGTCAGCTGCTGCCAGTGCCACAG[G/A]TGGTCTAGCCTCATGG CAGAAGCATTTAGCCAACTCCTGGTGTGCTCCACTCTCTTCTTCCGCCGCTGGGGCTCACCACC TCTTCTCCTCAATC
WI-16824b	83 G A ---			GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGTTGTTCTTATGAAGAAAGTCAG AAGCTGATAAAGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCTGGTCCCAAGTGGGTGTGGA GCCTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTG	CAGCTTCTGAC TTCCTTCATAAG AA	GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCTGCAGCTGTTGTTCTTATGAAGAAAGTC AGAAGCTGATAAAGTGGGCTTACACCTTTAGCAGGATAGTTTCTGGTCCCAAGTGGGTGTGGA CTTCCATTATGGGAATA
EST16445 3	96 T C ---			TTGCTTTTATTAAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTTATTATTACAAA AATGGCTTCCAAACCATTAATAATGAACTT[C]GGAATAAGAGCATAAACGGAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCACT	TATAATCCATCCTCCAAACACACACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTTCCCAA TTCACAAGACCTGTGCTTCAAAATGTTTCTTGATAATGTGGAGAAATCTGCTCTTTAIGTA

WI-16879	79 C	GATACAGGC T ATATTCCCA	CAAGGCTTCT AGAACTAGAGT CC	AGACAGGTCAAAACAACTCCTAGGGATAAAGATATAATCCAGCACAGCATTATTTCCAGATACAG GCCATATTTCCCA/C/TATAGGACTCTAGTTCTAGAAAGCCTTGGGGAGAACAGGCACCCAG
WI-16882	99 A	GAAATGCCA GCGTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGGTGGGAGAGACAAATTCCTCCCTTTACCCAAAGGTTACTCTGAC AAGGCTATGAATGAAAATGCCACGTCTCTGAC/A/G/GCGATTACCTGACATGTGTCATCCT
WI-16888	70 G	GCTAATTTGG A GCAGTTC	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAAATGTTTCATCACTACCCGGGGAGAGCAAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC/G/A/TTAAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75 C	ACTGGCCTGT T GTTGTCA	GTCTATACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTGCTCCCAACATCAGAACATAAGTTCCATGAAAACAGGAACCTTTGGCCTGTG TTGTTCA/C/TCCCACTGCCTAGAGAGTAGACA
WI-16910	74 G	AAGAGTAAAG ATGGCGCTAG AA	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTGCTTAAGGAGGTTATATTGCTATGACTTTTCATCTCAGAGAGTAAGATGGCG CTAGAA/G/A/GTATCTGTTATAGAAACGATACCTTCAATTTGGGCTGAAACAGTGAAGGT
WI-16918	93 C	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAATAAACTACCACCATCTCTCTGCTACCACAGAGCACTAAAATCTAGGAAATTTGAC TTTACTGCAGCCATTAAACACCAGCAC/C/T/GATGCCACTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127 A	GGAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTTCTATGGAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGG/C/C/CA CGGCAATCACATGAGATG
WI-16947a	58 C	CATGGAATA GGCCTGGAG ATCCTGT	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTTCTCATGGAATAGGCCTGGAG/C/GIACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGGACCA CGGCAATCACATGAGATG
WI-16966	43 T	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTTACTTTAAAATGCACACTACATAACAACCTAATA/C/CTTAACTTGGTCCAACCTATT AGTATAACTAATAGATTTTATCTGATAACTTGCAATGCCATTAAA
WI-16995	55 T	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATTT CCAGCGGT	TTAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAATAGTATTT/C/JACGGCTGG AAATCAACATGCCTCTTCTCTGTGAAGTTGTACGATGGAGCTGAGAAGGCTGAGTCAATCT
WI-16992b	60 T	---	---	AAATACATGGTGTCAACCTCAGCTAAGCAGCCAGAAAGTACACTGTGCGCCCTCATCTGAGAT/G/GTG TAGGACTGTAAGGGAATGTTTGGGGTTAGGAA
WI-16992a	46 G	AAGCACCAG AAGTACACTG TC	CACATTCCTT ACAGTCTTACA C	AAATACATGGTGTCAACCTCAGCTAAGCAGCCAGAAAGTACACTGTG/C/AJCCCTCATCTGAGATGTG TAGGACTGTAAGGGAATGTTTGGGGTTAGGAA

WI-17010	23 T C	T T C A C A G G A	A A T A A T A C G G T	A T G T T T C A A C A G G A A A A G C C A T G [T/C] A T G A C A T T C A A A A C C C G T A T T A T T A G A A G C T C A T T T A A T
EST17127 9b	74 C T	C A C T C G G C A C A G A C A G A T	G G G A G G C A G G G G T G	T G T T T A A T G C A G A C A A A A A T C A A G G C T A A C T A A A G C A G A T C C A A T G A C C C A G T G A T C A A C C T A G A G G T C C C A C G
WI-17040	94 T C A	A A T T C T C T T A T C A T C T C A A G C C	G G A C T A T G G C T T A T T C A G T G A T G	A T T C C G T C T C A A A C A G C A T C C C A G G C G G G C A T C C C C C A C G A T T T T A T A A T A C A C T C G G C A C A G A C A G A G [T/C] T T G G A G C C A T G G G C A C C C C T G C C C T C C C A G G C T T C C T A A G T A A C A A C T C A C G C G T T C A T T A A T T G G T A C A A A G C A T G A A C A C T C A G G A C A G A T T G G C A C A A T A C A T G C A G T T C G A G A A T T C T C T T A T C A T C T C A A G C C A G [T/C] C A T C A C T G A A T A A G C C A T A G T C C C A G T C T G T T T T C C A A A T C T T T C T C A T A T T G T
WI-17044	47 T G	G C C A A G G G A T T A A C G T A T A G	G G G A T C C C T T G T T A A G A	T T G T T T G T T T T G T T T T C T C C T C C C A A G G G A T T A A G T A T A G G [G/T] C T T A A C A A G G G G A T C C C C C A C T T A T A G C T G A C A G C A G C A G C T G C A A C C A C T G A C T C T C C T G C A G A A T G C A G G A A T C G A A T C A A A A G A A A A G C A A G T G
WI-17021	62 T A A C T C	T G G A C T T G T C A G C C T A T A A C T	T G T A G A G T T A G T G C A G C T C C	G C A T G T T G G A G C A G A T C C C A T G G T A A G C C A A A A G T G G A C T T G T C A G C C T A T A A C T A C T C [T/A] G C A G C T G C C A C T A A C T C T A C A G G C A C A G T A A C T A C A C T T T A T A C A G G A G C A C A T G C C A A A G T G C C T G G G A G G T G C C A T A A A A T C A A
WI-17065	90 T C C T T	C C A G A A A G G A A A A G C A T A A A	C C C A A G A G A C A A T G A A A T C C T	T G T A A A A A A T G T A G A C A T G G G G A A A A A A C A A C T C G T A A T C A A C A T G T G C T T T T C T A C T T C C G G T A C C A G A A A G G A A A G C A T A A A C T [T/C] A G G A T T C A T T G T C T C T T G G G T
WI-17066	32 A C T	T G T A C A G C C A A C A T C A C T G T T	G A G A T G T T G A A A A T G T T C T G G A A	T T C A T A A G G T T G T A C A G C C A A C A C A T C A C T G T T [A/C] A T T C C A G A A C A T T T T C A A C A T C T C A A A A A G A A A C T C T G C A C C C A T T A G C A G T A T C C C T G T A G C T T C C C T A T A G G C A A T G G C A A C T G C T G A T C
WI-17074	86 T G	T G C T G A C T G T C A T G A C T T A G T A A G G C C A T C A C A G G T T G C C A G A A C A T C T A C T C A A C T G T T C C A A G C A T A A C C T C C T A C A C A G G C C [T/G] C A C A T A G G A G T A T A T T T G G C C A A G A C T C A C C A C T A G A A G T G A T T
WI-17104b	108 T C	C A G A T G A A A C T C A T G C T G G C T C A T C T G C A A G C T T C C T G A T G C T T T G C G A G C T T T C C C A T T C A T T C C A A A T C A G A A G C A G T C A G T G G C C C G T G G T T C C A G A C G G C [T/C] T C T C T T T G T T A A G A A A T T A
WI-17114a	37 T C	T T T C C A T C A A G G A C T T T G T T T	T T G T A T T A T A A A T A G C A G A G T G A A G A G A C	A G C G T C C A A C A G A T G T T C C A T C A A G G A C T T T G T T T [T/C] G T C T C T T C A C T C T G C T A T T T A T A A T A C A A G C T A C C T C C C A A G G C C A G A T G C T A A G T G C T A A A A G A A G A C T G C A G C C A A A T C A G A G T T A C A T G G G A
WI-17150	76 T G C T C T T	G A T G A A A T T C A G A T A G T C T T C	T T C T C A G A A T C C T G G A A G A T A T G	C G T G G C T G G A C T A A G T G C T C T T T C C A T G T G G A C A C A T C T C A C T G A A C A G G A T G A A A T T C A G A T A G T C T T C T C T [T/G] C A T A T C T T C C A G G A T T C T G A A G G C C T C C T T T G T C T G C T C T A A T T T
WI-17163	43 A G T A A C G T T	C A T T T C T T T G T A A A T A A C A A	C A G A A T C T T G C T T T T G C C T T	G A A A T C G A A T A C G T C C A T T T C T T T G T A A A A T A A C A A T A A C G T T [A/G] A A G G C A A A A G C A A G A T T C T G T A A C C A A C A T T G G A A A G G G G A C A C A G G G G C A G A G G G A A G G G C C A G A T T T T C A A C G G T T T C C T C C A C A T C T G C A G A C A A A

WI-17178	127 T C	GGACTCCCTCA TGAGGAGC	CCCTCAATTT CAACTGCTTC	AGCAATGTCCCTCCAAATTCATTAGCTATGATGGAGTTATCAGTTTCATTCAGAGGGAATTACTGG GGCGAGGGGGTTTAATATCTCTGATGGGTTTAATTCAGTGAGGACTCCCTCATGAGGAGCTTC/JAGAA GCAGTTGAAATTTGAGGG
WI-17180b	81 C G	---	---	TCATGGACATCCTGAAGGAGACACAAAAATATAGAGAAATCCTGCACATTCCTCAAGTCTCGTCGACAG GCTTCAACAAATTAC/C/GJAACATCTTGCCCATTTTGTTCATTATCCGACCCACACTGACAGATGAG GGAGTC
WI-17180a	47 T C	CACAAAAATA TAGAGAAATCC TGCA	TGGGACGAGAC TTGGG	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACATTCCTCAAGTCTCGTCGCA CAGGCTTCAACAAATACCAACATCTTGCCCATTTTGTTCATTATCCGACCCACACTGACAGATGAG GGAGTC
WI-17156	54 G C	TGTTCTCTAAA CTTTAGATATC TCCCA	CAAGAAATAT ATATTTGATTC TGTGGAA	TGAGGTAGCAGGGCATTCTTAAGAAATGTTCTCTAAACTTTAGATATCTCCCATTC/CJTCCACAGA ATCAAAATATATATTTCTTGTTGGAAATTTAAATGTTCTTAACATATCTGCCTACCATCCACCTCAAT TAATATCTTG
WI-17149b	79 T C	---	---	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTCATGCACGTGCGTGGAA ACCCAATTGTCA/T/C/GTGTATGAACACTACAAAAAGGATGGGGAAGAAACACATTTCTCTACA CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATTC/GJTCATGCACGTGCGTG GAAACCCAAATGTGCTGATGTATGAACACTACAAAGGATGGGGAAGAAACACATTTCTCTACA
WI-17197	67 G A	GCAGAAGTAG CTGGGGCTAC	GGTGAGGTGGT GCATACC	ATTTGCTATGTTGCCCTGGGCTGGACTCCAGCAATCCTCCTGCTCAGCAGAAAGTAGCTGGGGCTAC/G /AJGGTATGCACCACCTCACCTGCTTATCAGTTTCGTTTAAAGAAATATTTGACTTTTAGATGCGCA TGATTTTCAGTACTTTTCTCCCTTGTCCCTAGTTT/C/JTAAATTTCTCAGTGGACAAATGGACAA ACCATCTGTTTGAATTTGAATATACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC TTC
WI-17198 EST18753 8	38 A C 27 C T	CCTAGTTT CTACCCAGGCT GGTCTCAT	ACTGAGAAATT GGATCGCATGA GCTGA	TCGCTATGCTACCCAGGCTGGTCTCATTC/JTCAGGCTCATGCGATCCTCCTGCTCTGCAGTGGCTGG GATAAGACACAACCTGCCACCGCCTGCCCTAGGAGTAGTCTTAATGCCIGATGGTGGG
WI-17108b	74 C T	GCCATTCAGTC TCAAAAGTAA CA	AACTACGATTT ATCATATGCTC CC	TTATTTTAAACATAAACAGATGCACCTTGGTTTTTACATTCCTGTTGCCATTGAGTCTCAAGT AAACAC/C/TJGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCACCTTACAGAGT ACACAAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCA/C/GJTGCGCATTAAGTACATTTCAACT TTTTGAGCAACCCGCCATCACCATTTCATCATCCATCTCCGTT
EST19067 2b	41 A G	---	---	ACACAAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTTC/C/JAGTGGCATTAAAGTACATTTCAACT TTTTGAGCAACCCGCCATCACCATTTCATCATCCATCTCCGTT
EST19067 2a	40 A C	CGTGACCATT AAGGGTATAG TTC	AAAAGTTGAA TGACTTTAATG CCA	CTGTTCTCAGAGATGACACTGCCAACA/C/GJTCACAGATTTTGCATACAATACAGTTATGTATTGGC TATTCACAAATTACAGTAGTGTGTTTTTCTCTGAAAAA
EST19125 8	28 A G	---	---	

EST20824 8	115 T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCGA	GTGTGGAAGCCGGAGTTTATTATTATTCAAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGGTAGAGGGCCAGTAAGTCGGGAGTGGCTGATTG[T/G]TCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50 A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCAGATGGGTGCATCCTCAGAACTTCTCAGCCT[A/G]GTAGCACAAAGTGG ATGCTTGAAGAACTCAGTCTTGGAACTCAGACAGCAATGGAGACGGGATGTGAGTGGGACCA
EST21904 b	128 G A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTT AGAAAGCAT	TGATTGTGGTCTGGGAGCAGGTGGCGAGTTCAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTCATATGGCCATTTTAAATAAGTG[G/A]TA TGCTTCTGAACACCTGCC
EST22111 3	82 T C	GAAGATCTGT CTGGCATTTCT	TGGAAAAACA GCCCCAC	CAACAAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGTCTGGCATTTCTT[C/G]GTGGGGCTGTTTTCCAAGGCACA
EST22197 2	78 T C	AATTATTCTGC TATTCCTGCCA	ACCATGAAGG ATGGGT	GTTTAATGATCACTCACCAAAATCCACAGGAGAACTCTTAAATGTTTACAAGCACCAATTTATCTGCT ATTCCTGGCATT[C/G]ACCGCATCCTTCATGGTAGAGTATCACAAGTAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T C	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCATTCATGGTTTACTCTA[T/C]GTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACITTCATCATCCAG
EST22311 9b	54 A G	---	---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCC[C/G]CCACTGTAAA CAGTAGCATTCATGGTTTACTCTATTGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACITTCATCATCCAG
EST22311 9a	41 T C	GGATTAGATC ATCTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TCGAGGAGCTCTGAGGAG[C/G]CACCAGGGACGTGTGTCAGGGCCACCCTGCAGGCAAGTGTG GTCCAACTCCTTCCCTTTACAAAACTCCAGCCTACCCACACAAACACTGGCTGACAGGCCCTCT TAAGCCTTTTAACTGT
EST22319	19 A C	---	---	GATGTTAATGACTTTCCCTTTGAGATATGATGAAAAATATCCAGGTACACATGGAAGACATGTT CACCAGTGAACCAATCTAACCCAGAAAGCTTTACC[A/G]TCTGTCAAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22433 c	103 A G	AAGACATGTT CACCAGTGA AA	CAGCTTCAGCT TAAGTACAGA AGTTTCAGTTT GCATGAATTT	TATCCATTTCAAGAAAAAATGACTTAAAAAATACAAATCTATCCAGAAATGGATCCTTATCTG CACA[A/G]CCATTGAAGAAAAAATTCATGCAAACTGAAACTATGCTTT
EST22657 9	71 A G	AAATGGATCC TTATCTGCACA	---	---

EST22993 5b	71	T C	ATCCTTTTGT TCTACCCC	TTGCTGTAA TTTGACTGTAA TG	GCCTTTTATTGCTCCTTTTAAACATCAAAATGTTTTATAACACACTTGATCCTTTTGTCTTCTACCCCA ATT/C/CATTACAGTCAAAATTACAGGCAATATAATAGGCTAACAGAAATGCTTGCAATT
EST23021 0	108	T A	---	---	TTATTTCACAGCTTACCATTGTTGTACTTATCTCTGTACAAGGTGTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAAATTTTATTAAATCTTTGCCCTT/C/ATAGGTTTTGACAGTTTTGTGCTCTTCT T
WI-17387	55	C G	CCTTTCAGAT TGAAGAAAA	GCCTTTGCCTA AGATTAATAGT AACTACT	ACAGAAATTTAACATGCAAGTTTCATTTACATTTACCTTTGCAGATTGAAGAAAAA/C/GJAATATTAG TAGTTACTATTAAATCTTAGGCAAAAGCCATTTCTTTG
EST23669 1	101	A C	AATGTAAGCT CCAGAGGCAG	OCCTCCCTCC TGTAAGC	TTTTTGGCTTGCTGCAGAAATAGATGAAGAGAGAAAAATATACCCAGATACCTTTGCTCACTCTCCCA AGTGCACACTAGGCAATGTAGCTCCAGAGGCAG/C/GCTTACAGGAGGGAAGGACGCTGAGGC CAAGAGTGGCTCACTG
EST23733 9	31	T G	GGCTGTAGTT TTGTTTTGTT	TGCACCTTAA TCCCATCAAT	AAAGCTGTAGTTTGTGTTTTTCTT/C/GJATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAAGGCTAGAGAAAGATATGAGGCCCGAGAGAGAGGCTCAGAGATTTCTAGAGGCGGC TGAAGAATACCCACCTAA
WI-17470	83	A G	GTCCCGTCCG CCAG	CCAGTGACGAG GCGA	CTGACACGTCCTGTGCGGGGGTGCATGTGCGGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCT/C/GJTGCGCTCGTCACTGSCCTTGCTGACTTTGTATTTCTGTCTTGGTTGGAA TACCATTACGCTTCC
WI-17519	55	T C	GTGTCCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAAAATGCATTTGTGCTAGCTAATGAATGCAT/CJAGAGTATTG CCTGCAAAATATAATTGAGATTCTATTTTAAAGAGCTTAGAAGAGTACATGGTGCAATAG
EST25356 3b	95	C G	---	---	TCTTTGATACAGGTAACCAAGTTTGTAAACATTTTCAAGCTTCACTGTATCTTCAAGTTTTTGATAT CAGCATCTCTGTGGAGAAAGCAGTGTG/C/GJATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26	A C	---	---	TCTTTGATACAGGTAACCAAGTTTGT/CJACATTTATTCAGAACTTCACTGTATCTTCAAGTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99	C T	---	---	GGGTGACGCTCCAGAAATGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGTATAATGATAGAACCCAA/C/TJTAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86	T C	ATTCAACATT ACTACCAGTT ATTGCGCT	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAAATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGTATAAT/CJGATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86	A G	ACTTCCCTGTG TAAACACTCC	CATTCTTATAG CTAGAAATCGA CAATAT	GTGTGCTGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAGGCCTACT TCCTTGTGTAACACTCCC/C/GJATATTGTGCGATTTCTAGCTATAAGAAATGGGCGCACTAAGTGGGTC

WI-17623	46 T C ---				TGTGGTTTAAATTTAAATTTCCCATATAATTAATGGTGGGCACATTTC/GCATGTGCTTACTGGGTC ATT CATATATCTTTTGGAAGCATCTGCTCCAATCTTTTGCTGACTTTGGAGTTTTTTGGT
EST26419 1b	46 T C ---				ATTTACATACAGAGATACAAAGCAACTATGTGCAGCAACAATCTGATTC/GJGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	35 C A AG	ATACAAAGGC AACTATGTGC	CAAGAAGTTTG GACTGOOC		ATTTACATACAGAGATACAAAGGCAACTATGTGCAGC/AJAAACAATCTGATGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTAATGTCATGATGGCTGGTTCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780 5	69 G C ---				TCAGCTTTAATTTAAGGGACATGTAATAAAGATGCAATTTGACAGGACAGCAGACTAGTTCAAGC AG/GC/JAGGTTAGACCAGTAACAACAACCAAGAAAGCAAAGTGCTCGTTTCCATCTTGGCTTTACCA CACTTACAACTGATACCC
EST26900 7	39 A G ---				TACTTCAGTTTAAGGCAAAATCCACACAGAGACTGTCTC/A/GJGAGACGGGCACAGAACCCAGACACC GTAGAAACACCACCACCACCATGTCATGACGGGGAAGCAGAG
EST27152 1	101 C T ---				CAAGGATTTTATTTTGTCCCTAAAGTAAATCTAGAAAATAGCAACCCACTGCAAGAGAGATT CTATACATAAACATTTTCAATCATCTCTCTCTC/JTTTACATGGTGTACTCTTTTCATGTACACAT CATCGGAAAACAGACTGA
EST27504 0a	33 G A ATTT	GCACTTTGCAA CAATTTAATA	GCTGGTGTGAT GCTACTGTAAT G		TTTTTGCACTTTGCAACAATTTAATAATTTATC/G/AJCATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGCTTTTCAGTATTTCTGTACACATCTGTGTTAACAAAGAACCCATACATT GGTAAATTCATTCT
EST27662 4	51 C T CTCCAGTCTG	CACATTCTGTT CTCCAGTCTG	TTATGGAATG GCTTATGTAAC C		ATCTTAAAGGACCATTAGAAAAGGCCAGTCACATTTCTGTCTCCAGTCTTG/JAGGTTACATAAG CCATTTCCATAAATTCATAGCCTTCTTCTTAGAGTAACACACACACTCTGTTTAGGAATGTTT
EST27788 3	100 A G ---				ATTTTATTAGGCGGTACAAATTCCAAGGTGGTAAGGGTGAAAGGAAAGGCGAAGGCGAGGCAATACAT TATTGAGCTGAAAACAACCTTTACATTTCAAGGAC/A/GJGCTTCCAGACAAGCCATGTAGAACCAGCAT GCCITGGGACTGTGTGGAT
EST27828 4	58 G A AGAACCCAC	GGAAGTCATC AGAACCCAC	GTGCAGAGAGG TACTCCAAGTA C		TCCTTAAACTTTCTTCTGTGGATCCCAAGTACGAGTGGGAGTATCAGAACCCCACTG/AJGTACTT GGAGTACCTCTCTGACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58 G A ACAATC	AATAAATTC AATCTGTCAC	TCAAGAAGGCC TTATCCATT		TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTACACACAATC/GAJAAATG GATAAGGCTTCTTGACAAATTTTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC TCCGCTTCCAAAAGCTTTATTGGCAATATGCTCTAT/CJAAAGAATGATCAATCCCTGTTGCCTCT AAGTCAATGGAAATGAAGAGCTGTGTCAGGGACACACACCCGCTGCTGAAGGAGACTGCTGTTGTG TCCACCTCTTATTCATAG
EST28036 4	37 T C ---				

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT TTAAA	TTTCTCGCAT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTTCTTCTTTAAAT/AJATGGTATAAAAAATAAATGCGAGAAACATTAAAC GGAGAAATGTACAGACAACAGACGAAGACATGAGTTTGTTCTGACTGTGACACATTTGGTGAAA
WI-17724	50 T C	TGGGOCCTCC TGTC	TGGGTTGGCAG TGTC	AGAAATGGTCTAGTAATCGTTCCAGGATTCGGTGATGGGCCCTCCCTGTCT/CJGGACACTGCCAACCC CACAGCTGGAGGGGCACCTTAAGGCACGTCATTTGTGATTAGA
WI-17730b	68 T C	---	---	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGTATAGTTACATCATACCAAGTGTACATACTG TT/CJACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTAGTGTGTC
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACCACAGAAAGTGAAGTGTCTATT/CJGTTACATCATACCAAGTGTACATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTAGTGTGCA
EST29041 5b	53 G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAACACACATTAAGCATCATTTGTCACCT/GA/GCTAACTCCT CAAATCAACAATACCCCTTATTTTAGCCATGAAAAC
EST29128 4	58 A G	---	---	CTTTAGAAGGACACCAGTCTGTTGGACTTAGGGCTTACCCTATTCCAGCAGGTGCC/A/GJTTATTT TCACITGGTTACGTCGTGAAGGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTGTCTGGGACACT
EST29912 3	103 C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTCTTCTG T	ATTATTAGGTAATCTGCTGTTGGGGTGGGGTGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCT/CJACAGAAGAAATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	---	---	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAAGTTAACTCACCATTGAAA TTTAAACCTTCTGTAAGTGGCTTCACTGATGAGGCAGTAACTACATAGGGATAAA/G/CJAGCTCAGTA TCTGGAATCATGCTTCTG
EST30223 2	99 A G	---	---	AAATAAATACATCATGCGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTTAATAATTC/CJ/GGATTTAATTTCTTCTAGTTCAATCTTTGGGA GG
WI-16260b	86 G A	---	---	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAAGAAAGACCCAGA GTTTCACAATATAGGTAGC/GA/ATAACCAAGGCTCACCTTCCCTCCGTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAAACTCTG GGT	CTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAAGAAAGACCCAGA AGAGTTTCACAATATAGGTAGCGATAACCAAGGCTCACCTTCCCTCCGTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGTGCTTTCTTG/GA/GCCTGTTTCTTATACCCCAATATCATAGAATT GTTGTGCTTCTATATGTTGAGCTTCAAAATCTTTTGCTTAATCAATCAAAATGAATTACCTGAATT TTCTCCTCTTGTTCAAAA

EST31951 4	87	C T	GGGTTGTCCAG CCAACA	CCACCCAAAT CACTCC	ACAGCCATTATTATGTTTACTTGGTAATATCAGAGACTGAAACATTTTTCACCTCTTTAGCAATGACA TCGGGTTGTCCAGCCCAACA/C/TTGGAGGTGATTTTGGTGGGAATTCCTATCACAAATTATTCT
EST31968 8b	95	T G ---		---	CGAATTTGTCTCTCTTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGCGGGTACTATAAGT GCAATTTTATAATGGGATTTCTGCTT/GJA/ACTGCCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST31968 8a	75	T C T	GCGGGTTACTA TAAGTGCAATTT	TGTAAGAATCA GTGGGCAGTT	CGAATTTGTCTCTCTTATTTTGTGATTCTAGTAATCCTAAAGATTTGGGGCGGGTACTATAAGT GCAATTTT/CJATAATGGGATTTTCTGCTTAAGTCCCACTGATCTTACATGGGAAAGGTGCAAAAG ACAGTGGTACTGCTCC
EST32063 2	103	C T ---		---	TCCATGGATGAACAGACGCTACCATGCCACATCCCACCTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGT/C/TTGTTCAAGGCCCATTTGAAATAGCAAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65	A G ---		---	AAGGCTTCCAAAGCATTCAAAGGCACTGGGTGTTGTGCTCTAAGTTTCTGGTCACTGCAGCCCCA/G TTCTGTATTAGGAGACACCCCAAGCCAGTAACAATATGGTCTTGCAAG
WI-17800	29	C G GAGAAACTCA	GGGAGCACAA GAGAAACTCA	TTTCTTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACT/C/GJAAGACTGGGATTAATTGTAGGAAATATTTTCACAG TTTCCACAAGTCAGAGAGCTAATCCCAACCCCTCTGTATCTGGAACATACACTGCTGCCATTTCTGCG CCATGAAGGGAAATACCC
WI-17857	34	T G C	CCTAAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG T	AAACTGTCTTCTTAAAGTCTGGGATGACTTTCCCT/GJA/TTCTACATCAAGTAGAACCTAAGCCAAAT TCAGAAATCAGAAATCCTTTTGTCCATCAAAATCCAGCTAACTCAAGCTGAATTAATGTTTCATTTCT GTATCTGATGTAGTTAACCATGGCCTGTCATGATTAATTGCTATAAGGAAGGGAACAAATCTTTA TAGTGCCAAAGATAATTAATCTTGGTTTAAATCTTTGCCAGCAAAAGCAAAATAT/AJCCGACTGAC TGCTCCTTAGTCTGATC
WI-17860	121	T A AGCAAATA	TTTGCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	CAGCAACCTTTTGTGTTTATAGCCTACTTCTCAAAATTTGT/A/TTTGTGTGATTAGTGACAACG GGGGAATCTACAATGCTCAGATCACAGTAACACTAGCA
WI-17866	43	A T ATTGT		A	GAAAAAAGTCAAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCATGATC AATCGCCACGAGA/G/AJACTGGATGCCAAAGAGTATGG
EST33301 4c	80	G A ---		---	GAAAAAAGTCAAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCCTCACACAAGCAT[G/A] ATCAATCGCCAGAGACTGGATGCCAAAGAGTATGG
EST33301 4b	63	G A ---		---	
EST33460 1	44	G A C A	AGCGTGGTTTT CAATACTAAA	CTGTATTATT GTTAAATATTT GCATTGT	CTATCCAAAGATATTTATTGCAGCGTGGTTTCAATACTAAACA[G/A]TGTAAACAATGCAAAATATT TAACAATAATACAGTGATTAATAAGCCATGGCATAATCCAGTTGATGTAATACTTTGCAA

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAAATAAAATGAACAC[AG]TACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACACAAACACAAATGA
EST34149 5	69 A G A T	TGCCAAATAC TCAAGTGTGA GAT	AAGTACTAGCG AGAACAACTA ATAAAATC	GTITTTTCTTTGAGTGACACAAGCTTGTTCAATTTTGAGAAATGTGTGCCAAATACTCAAGTGTGAA T[A/G]GATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATTCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C A ---	---	---	TGGGAAACATAAGTTAACTCAAGAATATATCCAGTCTTTATGTTACTAAACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCT[C/A]TACAAAGATTAAAGAAACTTACCATCAAAACACTTC CAGTGCATCAA
WI-17982	98 C T C C T A A A A G C	GGACCATATG ATATATAACT CCTAAAAGC	CAGAAATTATG TGATAATAACT CCTTCC	GGTACACAATTTTAAATGGAGGAACACACAGGTATGTTGAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATACTCTCTAAAGC[C/T]GGAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118 A C ---	---	---	CTCAGTAACTCCGGTGTATAATCTGCCATTTATTGATTTATTATGATAAAACACCTCTCATTTGTGA AAAAACAGCTAAGGTGACATCTCCAGACCACCAACACTGTCCCTGTAATGT[A/C]CTGCTGAGAGTCC ACATTTTGGAAATCCAAAT
WI-17996	84 A G A G G A A C A G	GTAGAGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGGTGGAGCAGCATGAAACAAACATCTCCCAGGCCCTCGCAGT AGAGGCGAAGGGAACAG[AG]GCTGCCCATGTGCCTGTCTCTAAAGACGCCACCTCAGGTTGATGT CACCTGTGGGAGACCGGGT
WI-17136	33 C G ---	---	---	ATTCTTTATAAAACACCATGTCCCTAAAATGT[C/G]ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCT
WI-18041 EST35164 8a	24 A C --- 57 A G C C C C	CACAGCCCTGC C C C C	CCCTCTGGATT CTGAATCTCAA	GCCACTGAAAAAAGGTGCTCTTCC[AG]GTTTCTAACTCCCTGACTCCCTCATTTGGAACCTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACTTAATCA
WI-18052b	67 A G ---	---	---	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTTCAAGCACAGCCCTGCCCC[AG]CTTTGA GATTCAGAATCCAGAGGGTCTCAGTCTTGTTTAGGTGCTCTGTGACATTTCTCTTTG AGCGAATGAAATGCTACATAGGCTCCCTGAGTCTTTCATGTACGAATCTTGGTTACACATCTAGI A/GIACAGCAGAGCTGCCTGAGGAGGGTGTGTTTAAATGTCGTATGCATGCTCAGCACAGTGTGCTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C A T C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCTTTCATGTACAGTCTTT AGAACAGCAGAGCTGCCTGAGGAGGGTGTGTTTAAATGTCGTATGCATGCTCAGCACAGTGTGCTGGC ATGGCCCATCCATGCTTT
WI-18054	46 G A G A G T A A A A	GGGAGTGGG G A G A G T A A A A	CGTACCTGTC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAA[AG]TGAAGCAGGGTGAAGC CATGCAGGAGTCCAGACAAAAGACGGGTGATTTTGTCTCAGGTGGTAGCAACAGAGGTAATG

WI-18064	54 G A	GTAGCTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAAACCCTGTGGGTAGCTGCTAAGCTGTATTTTCAGATG/GA/GAATGTACAC AATCATACCACCTGGGGAGAAAGAGTAAGCACAGTGTCTATTAGGTGCCAAACTGGGTACCTGGGAG GCAGAAA
EST35347 2	97 T C A A	GCATAAAATT TTCCAGTTGGT	CCCTCGGCACC TGCT	TTTAGCACCATTCTTAGTGGAGCAGGATTCTTGATCATGGGTGGAATTTTGATATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT/C/JAGCAGGTGCCGAGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28 A C GTGTAT	AACCCACTAG TTACTCAGAGT	AAAACTAATA AGAAACTGGA GGTTTT	AAACCCACTACTTACTCAGAGTGTGTAT/C/JATATTAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATAGTTTGATATTTCTGTACTCAGAAAGCATTTTAGGTGCAAAAGGATATAA
WI-18080c	80 C T ---		---	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATACTACTATGCCGTG TTTGACTTTTATC/TJCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTTGGGTAT
WI-18080b	65 G A ---		---	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATACTACTATGCCG/G/ AJGTTTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTTGGGTAT
WI-18080a	41 T C AGTCTCTC	GCAAATATCA ATATCAAACT	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAATATCAATATCAAACTAGTCTCTC/T/CJTGTAAATTAATACTACTATGC CGTGTGACTTTTATCTCTTATGTAAATTGAAGCCAAAATGCATGTTAATCCTTCTCCTTTGGGTAT
WI-18086	63 G A ---		---	GTGGGCATCCTATAAAGCAGCCATGTGTTGAAACAAATGATATGCACAGAAAGCATCTTCT/G/A/ TGGCTTTGTTACACGGTTTCTTTCAAGAGGAAGATGACTAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTGAA
WI-18115b	71 C T ---		---	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAAGCCTTTAGTGTACCTTTGGTATCC TTC/C/TJTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCAATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115a	70 C T TT	TTAGTGTACCT TTGGTATCCC	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGCCTGGCTTAGAATCAATGGGTAAAAGCCTTTAGTGTACCTTTGGTATCC TTC/TJCTTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATACAATGTAAAGAAAGGGTGAG TCAGT
WI-18136	78 A G ---		---	TTTTGAGAAGCACTCTGTAAAGCAAGGATGCATTTCAAAAAATGGCTTTGAGGATTAACTTCTCTTTA GGTAAATTTGC/JAG/JTAAGAACATAAAGCATTTTAAAGTCCACTGCCGCCTTAGAAACT
WI-18169	115 A G GAAGCTC	CCATCTTTCCG	GAGTTCGTCTT GTGCTCA	GGCAAAATATTTTACATCAGACCTGGAATCTGCCCAAGTCTTCCAGTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTTATCCAAGCAGCCATCTTCCGGAAGTCTC/JG/JTGAGCACAAGCAGA ACTCGGTGGTAGAGTGA
WI-18190b	26 G A ---		---	TGAAAGAAAGTCGACACAGCGGACACT/G/JATCAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGAACAAAATCAAGATGAGCTGGAGACATTAATCCTGGCGA

WI-18190	62 G A ---		---	TGAAAGAAGTCGACACGCGGACACTGTCTAAGTGAACAAAGGATGAAGCTAATCATGGAG[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGACATTAAATCCTGGGGA
WI-18181	100 A C CAGATC	AAATATATAC AACACTCCCTT	CGTTTACCAT TTGTTAAGCTT TTG	GACAGTGAAAACATTGAAAACACAAATACAAACAAACATTAGGAACAAGAAATGTGTAATCCAA TGTTGAAAATAATATACAAACACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAAAACGTA TGTTCTTGAAC
WI-18215	78 G A CTGCOCTC	AGCAGAGTTC	CCTCCCTCTCT OOOOC	ATTATACAAAGCATTTCTGAGTACAAACTAGGGGACAGGTATTTACAAAAACAATAGAGCAGA GTTCCCTGCCCTC[G/A]GTGTGGGGGAGAGAGGGGATTTCAGCATTTTGGTGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60 T A AA	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGT C	CATTCGAAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAG[T/A]GAA CCCCTGAAAACCTTTATTTTGAATGAAGTTTTCCTCAGAAACTGGGCAGAACTTTTCACATTCTG AC
WI-17892	76 T C ACA	GGAAACTTG AGTTTGAGATC	CACAGAAGTG AATAGACTAGT GAGACA	TTTAAATGCTTAGATTTTCCCTCAGTATTTTATCAATAGTGTGAAGCTGGAAAACCTTGAGTTTGAG ATCACAATAT[C]CTGTCTCAGTAGTCTATTTCACCTCTGTGGGCATTTCGGCAGAAAGTGGC
WI-18242	30 G A AATCGTAACA	CCCCAAATGTT AATCGTAACA	GCTAACACTTC TACTGTAAACAG CTTTC	AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAAGCTGTACAGTAGAAGTGTAGCAAAAAAT TGGATGCCACAACCTTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTCTTGGCCTATATC TGAAAAGATCGAACAAG
WI-18266c	119 C T ---		---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C ---		---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T TTCAAA	AAATAGGAAA TATGGACTATC	TTTCATGCATCA TTTGTGCA	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACCTGCACAAATGATGCATGAATCCACATTTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G AA	GCTGCAGCTA TTGTTATTCA	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTGGATATGTGGTTTAGTGTCTATCATTAAATTTGGAAAGCTGCAGCTATTGTTATTTC AAAT[A/G]TATCTCTGCTCCCTTTTCTCCTTTTCTGGGATTCATTCGCGATGTGTTATA
WI-18330b	66 A G ---		---	AAACATCTACAGCTGCTTAGGCCATCCTGTGAAGAAATCAGGGGATGAAGAGCTGAGGAACAAGAGGG[A/G]TATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTTGTGTTGAT TCACA

WI-18330a	49	GA	AAGA	TCCTGTAAGA AATCAGGGAT	AGTCCTGACTC ACTGCCTACA	AAACATCTACAGCTGCTTAGGCCATCCTGTAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAATAAAGAACAATAATTTTGTGTGAT TCACA
EST37564 5	85	T	CAGA	AAATTCAAGC CATCTACAAA	CTATGGAGGOC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAAATGCTGGTTAGAACTACTGCATGTTATTTAAGCTAAAATTC AAGGCATCTACAAAAGAT[C/T]CTCATTGAGGCCTCCATAGGCTGCAACACACATCAAGGCATTAC TGTAAGTTAGGAGGAGGACTGAG
WI-18327	104	GA	TT	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAAGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGAGTTTCCCAAGCAGTACCTC CCAAACAATGGTGAAACACAGCTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATGCGGAGGCAGA GT
EST37624 6b	102	GA	---	---	---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGACGCTGATGG CCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACG[G/A]TTCATTCTACATGGCTGCTGCTTTGGGTCC TCTGACCTCCCCATTCC
EST37624 6a	58	CT	---	---	---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGAC[G/C]TGTGA TGCCCTGCAGTCTCTGCCGTGCTTGGCTCTCTGGACGTTTTCATTCTACATGGCTGCTGCTTTGGGTCC TCTGACCTCCCCATTCC
WI-18357	89	C	G	GCATCAA	AAGGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCTTACCGTGTGAGTGCCATGAAGCCAAAGCCCATGGAGAGACATTTTCAGA TAATCCAGCCCTTAGCATCA[C/G]TCATCTTCAGTCTTTGAGTCTTCCAGCCAGGTCCAAAGCTT GTGGACCAGAGACAAGCC
WI-18012g	117	A	G	---	---	TTTTATCTGGTCAGCTCCTTCTTAATGGCCTGAAGGTGTCATCTCCTTTCAACTTTCCAGACTTGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTT[C/G]ATGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	GA	---	---	---	TTTTATCTGGTCAGCTCCTTCTTAATGGCCTGAAGGTGTCATCTCCTTTCAACTTTCCAGACTTGAAG ATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTT[C/G]ATGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	CT	CCCTT	GCCACTTTTGC CCCTT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGTCAGCTCCTTCTTAATGGCCTGAAGGTGTCATCTCCTT[C/T]CAACTTTCCAGACTTGA AGATCCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCCCTT[C/G]TGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
WI-18012b	46	T	C	---	---	---
EST38390 4	75	A	G	CTCTGCATTG	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCATTGT[G/A]GTAATTAAGTTTATTATCAATCAGCTGACTTAGCATTTGGGAGATTATCTGGAT

EST38512 7	91 T G	TGACGATGCC AATACTTCG	CACTGCACTCT GGGAAGC	TAATAAAACTGACCCCAATTGGTAAACTGTGTCTGGACTGAGAGAAACAATGAAAAATCTGTAAT ACCTGATGACGATGCCAATACTTCGTTGJGCTCCAGAGTGCAGTGAATAACTGTTATAGCC CCTGCACCTCCTAAAAGATCTTTTC/TTCCCCCAAGTCTTAACAGAATGGTATATCTCTCTGGA AGATGAACGTCATCAATGGATTGTGCTGCTCTCGTTTCAGCTTTGATTTTTTGCTTGAGAACCTTG TCCTCCCTGCTGAATTT
EST38519 0	24 C T T	GAACATCCCA TGTTCTGTTT	AGGGAAGGTA GTATAACACAT AAGAGA	AGTGGTCAAAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACAATCCCATGTTCTGTTTAAJ T/CJTCCTTATGTGTATACACTTCCCTTTCTCTTTATACACATAGATTTTCCCTTAATTGCAGC CCA
EST38575 1	66 T C A A	CCTGCTOOGCC CTTC	GAGGAATGGAT GGTGGC	CCATCTAGGAGGCTAOCCTGAGCTCTCTGTGCTCCACAGATGGGTGCTCACGCCCGGGGCCCGGTGG AGTCTCGCGGGCCCGCCCTGCTCCGCCCTTC/GJGCCACCATCCAATTCCTCCAGGGG
EST38616 9	101 C G C T T C	TCTGAACTGGG CATTTCAA	TTGCAAAAATG AAAGGAAAAA	TATAGTAGTACTTTCTTCTGCTGCAGCAGGAATTTATTCAGTCTGAACCTGGGCATTTCAA[T/C]GCGTG GTATTTTTTCTTTCATTTTTTGCAAGTAAAAAATCAT
EST38652 8	59 T C	AATGGTCATTT TAATATATCA	CAGTGATGGTC CTTAATCTTCT ATC	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTTACATA[T/C]AGATAGAAGATTAAAGACCAT CACTGAGGTCACATAGCTCAGAGGAGAGTTAAGATTGGACCCAGGAGTTGGTTCCAGCATATA GGATCCTCACTCACTGGGACAGCCTGAGAAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCCGJAGJAGGCCAGCGGATGTGTGCCCTCTCTCCCAACTCATCTTTCCAGGAACACGAGG ATTCTGCTTTCTGGAAA
EST38707 9	75 A G ---		---	TGACCTTGATTTCTTCTACTAGAGGGGAGAAGAAATCACTACCTACCTTTTGGATGCCTCCCACTCTACTTGT CTCCCTGAGGTGATATGGJAGJCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAATTTCTTGCC TAGCAGCACC
EST38759 2	86 A G GGTGATATGG	AATCAATAGG AGAGGATTGG	TCACCATCGTG GACTTAAGG	GACTCTCAACCAAGAGAAAAATCAATAGGAGAGGATTGGCT/ATTTGAATTCAGAGCAAGCCCT CTTACTGAGAGGTGAGCCCGAGCCCTCCAAATGCCCTTTTCATGATGATAGGATCTCCTAAGTGGTAC AAACAAACCAACATGGTGG
EST38775 1	40 T A C	TGTTATGAGA ACCCATTACA	GGCTTTGCTCT GAATTCAAA	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTCACTTATGTGTGTTTCATTCACAAG TGTTTATGAGAACCATTACACA[C/A]AAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38815 4	91 C A CA	CACGAGTAAA AAGAACTCA	GCTGACTGGCA CATGCTTT	TCCTTACTGTGCTTACAACCTTCTCCTCAAGTTTGGGTGTTCCATATTGTTATTGTTATTGTTATTA TTCAACACAGAGTAAAAAGAACTCATGAC[C/T]TCTCCTTGAGCTCGCTCTCTCCCCAATCTCGAT ACCGACTGCACGTGG
EST38858 4	98 C T TGAC	GCTGTAGAATT TGATCGATGC	GGAGCGAGTCC AAGGAGAA	CCCTAATGGATTTACAGCTCATCTGAGTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTCG ATGCT/CJCTGTGTCTCCGCTCTTCCCCAATGAGCACATATGCAGGGCAGGCAAGAGCATGCTGGA TTTGCTTAGTTGTTAA
EST38865 2	72 T C		GGAAGGACGG AGGACACAG	

EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCTAA	CCTTCAATAAA TCTCATGTCT CA	CCAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAAAT/CJTGAGGACATGAGATTT ATTGAAGGGAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAAACATTCCC TTATCAATGTCTCATCTCACACATCTTTATTTATTTGTTTTCACACTTCTCAAATATCGGATTTGTC TCATGAGAATAATGGCTGAGGGAGCTGGCAGGCTCTCTCA/GC/GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	---	---	TTATTCAATGTCTCATCTCACACATCTTTATTTAT/CJTTGTTTTTCACTTTCTCAAATATCGGATTTGT TGCTCATGAGAAATAATGGCTGAGGGAGCTGGCAGGCTCTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTTCTTAT TTTT	CGATATTGAG AAAGTGAAAA CAA	TTATTCAATGTCTCATCTCACACATCTTTATTTAT/CJTTGTTTTTCACTTTCTCAAATATCGGATTTGT TGCTCATGAGAAATAATGGCTGAGGGAGCTGGCAGGCTCTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38909 5	47 A G	GCACAGCATG GCTAAAACG	GGTATTGTTG ATTCCCATCTT T	GCACTAAACTAACTTTTCATTTGTGGATTGCACAGCATGGCTAAACG/A/GTTAAAGATGGGAATCAA CAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT
EST38911 9	85 A G	GTGAGGGAA ACTTATAACCT CAC	TGTTGTTTTGT GAAACAAGCG	AACTGAATGGCAGTGAAACACACTACACATCAAAACTTAGGGAAATGTGGTTAGTGTGTACGTTGAG GGAACTTTATAACCTCAC/A/GJCGCTTGTTCACAAAACACAGACAGACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38955 5	30 G C	TGAATTCCTT GGTGG	CACTGCAATCT CACCCCC	TAAACATTCCCATTTGAATCCCTTGGTGGG/GC/GGGGGGGGGTGGAGATTGCAGTGTCTCAAGATAAA TATCACAATAATATCAAAACTTCAAAATTTGTCTATGCATTACACACTGACATGAGCCACAAACATT CCTTTCACAGGGACTGTAC
EST39002 0	42 G A	GGACCTTGGG TGACC	CTGGCAGGGAG CCTG	CCTGCTATGATGCCCTGGGAGATCCCGGACCTTTCGGTGACCG/A/CAGGGCTCCCTGCCAGGGCTTGG CCCCTGACCCGGGCTCCCGAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39004 8	79 T G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGGC	CACGTGGCCCTAAGTTCCGGGTCTTCTCAGTCTGGATGGCTGTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAATTTGJAGGGGCGAGGGGGCGATGCCCGCAGCGAGATGGTCTGTAAAGCTGTGGGTC AAAGACCTAACTTCTGGA
WI-16398	90 T C	TCCCTATTAT CCATGATATTT TCA	GAATGGTTGT GAAAAATATA TTGATAT	AAAGATAATGTCATCACACGCAACATATAGAAACATAAAAGAAAAATAAGTATCCACCCCTAAAT CCCTATTATCCATGATATTTTCAAT/CJAGCAACTAGTATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16403	69 T C	CCTTGTCTC AATTTTAAAC ACT	TAAGGGCTAAT TCCCTATATAA AAAG	GGTTGCTTTTCATGATTTTCTCATTTCTCATAGGTTTCTGGTCTTTGCTCTCAATTTTAAACACTT T/CJCTTTTATATAGGGAATTAGCCCTTAAACTGTGTGATCATGTGCCAAAAATTTCTCTCCAGTT
WI-16406	24 C T	GCTTAAATGGC TACAGAAAGA AGG	CCAGAACCAG ATGTGTTTAAA AA	GCTTTAATGGCTACAGAAAGG/CJ/GGTTTTTATTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTGCAATTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57 C G	TCATCTGAGA ATAAACTTCCT GTCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTTCATGTTTTCATCTGAGAAATAAACTTCCTGCTGCTAAATTTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAATGAATGAGGTGCTC TTT
EST39294 4	63 G T	CCTGAAACAG GGATGOC	GCACAATTAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGTACTATGTTTAAATTGTCTGAGCCAGCAACCCCTCGAGTTACCCGGCCTTTACCCACGCC AGCTCTGCTTGTCTGCAT
EST39366 2	72 T C	---	---	AGAAAAACATTCTGTCTGATCAGAGGAAGATGTATGTAGAAAAATCAGAAATCTGACTGAATTCCTAAA ATCTATT[C/J]ACACTGAGAGGAAAAATGAAAAAGAAATGTTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGGTTTCAGA
EST39371 9	86 A G	CATTGGATTA GCGTGAGAGG TT	TGATTTGAGAC ATTTACATTT TT	AAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTTATGTGTGTAAATCCAGTTGAGCAITTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAAATCAAATGCTTCTCTCTAAAGATTA GACATTGCCCAACCCCTGC
WI-17177	23 A G	---	---	ACAAGTGACATATCCAACCAAC[C/J]TCCATCCCCACCTGTGCCCTATTCTTCTTGTGTTTCTTT AGAGCCTTTTCAGCTATTCTCTGTGAAGCAAACTGCACGAAGGCCCTCCCCGCTACTCCTCCCTGGAA G
EST39428 8	31 C T	GCTCCACACA ATTTTGATT	GGTCCCTTATG AAGCACCC	AGGTTCTGTTGCTCCCCACAATTTTGATT[C/T]GTTGGCTTCATAAGGGACCCAGGATTCGCAAT TTCTGGTGGGGCCTAGGTAATTTCTGTGCCCTTTGGTCCACAGACACAAATTAAGAAGATCAGGTCT GGCTGTTCG
EST39430 2	45 A C C	GGCAGAGGAA TAACTGATGTT C	CAGGGTGCGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAAATGATGTT[C/V]CAATACCCCGACCCCTGA CCCAGTACCTTTCCCTCAGGCCCCAGGCTCCGGTGGAGGATGTCCTGGG
EST39446 7b	117 C T	CTACTGACAT AGGACTTCA GAGTAA	TCCTGGAAAAC TGACATAAAC C	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAAGAAAAATAACAGGAACCTATTATAT ACGTAATACACTTTCATACCTGCCTACTGACATAGGACTTCAGAGTAAT[C/T]GGTTTATGTCAGT TTCCAGGATTGTTCTCCC
EST39465 2	80 A G	AATGCAGGAG GGTGGC	CAATCTCGGCC CCTCT	ATGTTGTCATTAGAGGGCCACAGGGGATGGGGAGTAAAAAATAACATAAACGAACGAACAGAAA TGCAGGAGGGTGG[C/J]AGAGGGGCCGAGATTGGGTGTTCCAGGGCAGAGGTTGGAAGACCAG
EST39501 0	81 A G	AAAGATTCTT GTAGACATCT AACATTAG	CACITGCAATT CTGAAGGCT	TGCTTACAAACCCATAACCATAGGCCATGTGTTTCAGACATCTTGACCAAGCCTAAAGATTCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATGCAAGTGCAGTTCAAGTCAAAACCAATTC
WI-18387b	84 A C	---	---	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACATTTGTGGTCA CATGCTTAGCCATAC[C/V]CATGGTAACATTGACTATGGAGCTTGTGAAAAGTGAATGTGCGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CCTTACTTTGG TGACCCCAT	GCTAAAGCATG TGACCACAAA	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATAC[A/G]TTTGTG GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGTCTTGTGAAAGTGTAAATGTGCGATG GCTATGTAGACATAAAGA
EST40601 9	78 A G	GGGTGGAACTT GAAACAC	TTCTTTGGAAGA AAGGGTC	TCCAGGATGGTTTATTCAAAGCTGTGGACGGTGAACATTAAAGACGAAAGAGGTGACTGGCGTGGA ACCTGAAACAC[A/G]GACGCTTCTTCTCCAAAGAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32 A G	AGTGATCAC ATCTTCAGGAT AGGT	GCACACCTTC ACACTGTTA	TCCATTCAAGTATCACATCTTCAGGATAGGT[A/G]ATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTAGTAGAGGAGTCTCCCGAGAGTAGCAGTTGTGA
EST43091	28 C T	CATTCTGGTCT TTATTTTGGG CA	AAACTGATTT GTTAAACATG CTAC	ATGTCATTCTGGTCTTTATTTTGGACA[C/T]GTAGCATGTTTAAACAAATCAGTTTTCATAGGCAA CCTTTTGAACATCAAAAGAAATACAATATATTTTCAAAATTTCTCATCAGTGTAAATTC
WI-18420c	108 T C	TTCCATTAAAC AGGAAGTTTC C	AAATCTCAGC ATTGCTATAAG C	AGAGACACAACAAGAAGAAATAGGGGAAATGGGAAGACAGAGTGAATTAAGCAAAATCTTGA TTGAGATTCCATTAAACAGGAAAGTTTCTCAAAAAAATCAAA[T/C]GCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38 C T	GAATAAGGGA AAATGGGAAG AA	CCAAGATTTC TTTAATTTTAC TC	AGAGAGACAACAAGAAGAAATAGGGGAAATGGGAAG[A/C/T]AGAGTGAATTAAGCAAAATCTT GGATTTCAGATTCCATTAAACAGGAAAGTTTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101 T C	CACCCTGTCT AGACAGATTTC A	---	AGCTGATCAGCTGCTGTTACTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCCCTGTC CTAGACAGATTCAATGCAACAACAACAGGAGGT[C/GGGGGT]CACACGGCGGAGAGCCAAAGAC TAGGGC
WI-18425	81 A C	CACCCTGTCT AGACAGATTTC A	CCTCCTGTTGT TGTGTGCA	AGCTGATCAGCTGCTGTTACTGTTTATGTGTGGCCAGGGAAGCCAAAAGATCAGACACCCCTGTC CTAGACAGATTCA[A/C]TGACACAACAACAGGAGGTGGGGTGCACACGGCGGAGAGCCAAAGAC TAGGGC
WI-18449	129 C T	CTTTTGGCTCT AAGTGGGACT G	CTCCCTGACT GTATCCAGA	AAATTGAGGTCCGGTGGAACTATAAAAAGGAAAGGAAAGAAATCAAGGGAGGCCAAAGTG GGAAGCTGTATTGCTGATCTAACGTGCTTCCAGTTCCTCTTTTGGCTCTAAGTGGGACTA[C/T]TC TGGATACAGTCAGGGGAG
WI-18457	120 T C	---	---	ATCGTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGGTGGCCCCCAAGACATATTTTATTCTT AAATGTCCAATATCTGCCTGATGCTGTGTTGTGCACATTGGGGCCACAGT[C/J]AATAGGCTAAA AGGCAGTCCACCTGCT
WI-18462	39 A G	CCACAATGGC AGAGGTGA	TTTAGGCTTTG AGATGTTTCT	GGTGTATAGTGTGTACACCACAATGGCAGAGGTGA[A/G]TAGAAACCATCTCAAGCCCTAAAA TATTACCATACATCCCTCAGCAAAAGTTTGCTAATCTCGGTTTAGGGACTCCATTGAG
WI-18476	60 C T	GGTGGGGTGC GAGG	GCACGATGGGA GTGACC	TGAGGACGTGTGACAAGCTCAGAGGGGTGGGGCCGGCTGAGGGTGGGGTGCAGG[C/T]GGT CACTCCATGCTGTGCCCTGGCCGTCCCTCCACTCACCCACACCTGGCCAGTCCACGTTGAGGT

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WI-18491	109	G A	AACAAATGGT AGTGGTATT	CGTGTGCAATT TCITGTAAATCC	CTAATGAGATGAATACATGGAAGCGGTTTAGCACAGTGCCTAAACACAGTAAGTAACCAACAAT GGTAGGTGGTATTAAATACTATTATTAAATCCAGAATGAC[G/A]GGATTACAAGAAAATGCACA GGT
EST50757 b	79	C T	GAGCTCGAGG CTGCTTCT	ACCTTTACACC GOC	AGCCCCCTCCACTCCACTCTGCTTCCACAAAGTCGGCTCCGAGAGCTCGAGGCTGCTCTTTTATAT GTGACGGGC[C/T]GGCGGGTGAAGGGTCAGAGA
WI-17675	103	T C	GGACATTGG CATGGTGACTT	GGGGAACACC CAGG	GATCTTGGAAAGCACTAGAACTAACAATCTTACCAGGTGCTGAAGAAAAGTGTCTTCGTTTTAAT TGCCAAAGCAGGATGTGGACATTTGGATGGTGACTT[C/Q]CCTGGGTGGTCCCATAGATTACCAT TGCTCTAATGGTGCTA
WI-16543	67	G T	AGATAAACTA CAITTTGGTTT	GATTCATCAT ACAGGGACTT	GATCCATTACCTAGGGTAAATTTCTCTGAATGTCAAAACAAAGAGATAAACTACATTTGGGTTTTGG G/TJAAAGTCCCTGTAAATGATGAATCAAGAATCCTCAAGTCTGTCTTGCCACCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAGG TTGGGGA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAAACCATCTCCCCCTGACCCCATGTCATGCAATGGAATAATGTC TTCCACAAAACCCGGTCCCTGGTGCCAAAAGGTTGGGAA[C/G]TGCTGGTCGGTACAAAAAGTAATT G
WI-17690b	79	A G	AGGCATTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAGAAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTGATTT GGCTTCCCTAT[G/G]ATTACAGGACCAATACTCTTGTTCTCACTCATCTGCTATGCTGCTG
WI-17690a	63	G A	AGGCATTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAGAAGATATGTTGCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTT[G/A] TTTGCTTCCCTATAGATTACAGGACCAATACTCTTGTTCTCACTCATCTGCTATGCTGCTG
EST51717 b	128	C T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAATCTCAGTGTCTAACTCATCATCCAGATTAT[C/T]TGAAGTGGAAACCCCTCCGACCC TGCCAACATCACCCACTACCTGGTTTCTGGGAGAGGCAGCGGGAAGACAGTGAGCTGT[C/T]GAG CTGGATTATTGCCCTCAA
EST51717 a	39	C T	---	---	GATCCAATCTCAGTGTCTAACTCATCATCCAGATTAT[C/T]TGAAGTGGAAACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCAGCGGGAAGACAGTGAGCTGTTCGAG CTGGATTATTGCCCTCAA
EST53012	97	C T	TGGTCACTTTG GGGOC	GGCTCTGCOCA GOC	TTTCCAGGTTGACAGGTTTATTCACCCCTTCCATCCCCCATGGCCACCCAGGCAGGAGGAGACAG GTGTGCTGGAGTGTGGTCACTTTGGGGC[C/T]GGCGTGGGAGAGGCCACTGGGTTTACATTCTCTGT GGGACGTTGTGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTACATT TT	AAACTGCAATAAACAACAAAACAGAAGTCCAAGAAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCAACATGTAC[A/G]AAATGTGACAAGATATCCAGATGTTTAA
EST53389	74	A G	GGAGACCTGC AGAACTTAAA GCA	GCCCTTTCTAA CAATAAATGCT C	TTTCGAATGTCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAAT TAAACAC[A/G]GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAAATAGGTTTAAACATGAAC ACATTAAGGAGATGGCC

[illegible]

[illegible]

TIGR- A003P30	117 C G ---	---	---	ACAAGTTCAAAAGGAGAACTTCTCTTTGTTTAAATGCAGCTGTGCTCAGAAAGCCTGTGATTTCCCTAGGA AACCATCTGGGTTTAGCCATTAGCCATTAGAAAATGCAGTTTAAAGCAGTGTCA/C/GJACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TIGR- A004S34	156 C T A	TTAAA	---	GCTTGCTTTTATGTTAGGTCGGGGAAAGGAAGGGCTGACAAACCGCAGACATCTGGACACACAGC AAGGGTCCAGGGAGGTTGCAGAACTCTTTGCTCTGGCTAACAGTGTGTCATGTGACAAATAGCCA AACCTCCTCATTCCTATAAA/C/TJCTTTAACAAAACAGTTAGCTGTTTACAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97 A C ---	---	---	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAAGTCAAGGAGATAAAACCAAAATGAT TGAGTATGATAAAGAAATTTTGCATGGCGATT/CJAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAAGAAACAATATGACTTAGCAAAAGAAACAATATAG
TIGR- A004T44a	69 G A TGA	GCAAGATAAA CCAAAATGAT	GCCATGCAAAA TTCTTTATCA	AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAAGTCAAGGAGATAAAACCAAAATGAT TGA/GJATATGATAAAGAAATTTGCATGGCGATTAAATAGAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAAGAAACAATATGACTTAGCAAAAGAAACAATATAG
TIGR- A004V08	60 T C GGCACTCTCT	TCCTCCACCA AAAGGC	---	CCTACAATCCTATAATATTGCAAGGGTTGGGAAGGATGCAGGAAAACAGGCATTCCTTA/T/CJGCC TTTTGTGGGAAGGATCAATTTGGTGCATGCACITTAGGGGACAAATTTGGGCAGTAGCTGTCAAAATTTG AGTAGCTGTCAAAATTTCAAA
TIGR- A004V26	125 A G ---	---	---	TCCTAGCTATAAGACCAGATTTTAAATATCTAGATATAGAATTATCCAGAATAATCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA/A/GJAAAGGT TTCAGTTTATAAATGCTTAAATACTGTATCTATTGCTTAAATACTGTATCTATTGG
TIGR- A004V28 a	29 A G CGATCTC	CGGAGGTGCA GTGAGC	---	CCAGGCTATAATGTTGTGGGTGCGATCTC/GJGCTCACTGCAACCTCCGCTCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGACCCGCCACCGCACCTAACTAATTTTG TATTTTATAGTAGAGACATTGTATTTTATAGTAGAGACAGG
TIGR- A004X20	25 T C GA	GAGAC	---	TAAGTTTCCCTCTCTCTGTAGGA/T/CJGCTCCATGTTACAGTCAACTATAAAACATGGCTCATGT TCACCTCTGGGCTTCGCTTCAGAGGAGTTTGATAATTTTGGAAAGTGGTACCTTTGTTCTGTGCTTTTCA GACCAACCGCTTCTTTCATTTCTCAAGGCTTCTTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCTCT
TIGR- A004X30	26 T C CCAC	CTATTTT	---	TTTTGAAATCTTAGAGTAGAACCCAC/T/CJACTCTAGTAATACTTGTAAATAAAATAGTTTT AAACACTTCCATAAAGAAATAGGGGTGCCAGCTCCTTGATTTTCCCTTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102 T GATGCAAAACT	CTTATAATTAG AAATTTTCATGA AAGCAA	---	CACGGTATATGCCCTTATATATAGGTATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACTT/GJTTGCTTTTCATGAAATTTCTAATTAAAGG ACTGTTGCTTTCTTCATATTCAATGGACATTATACAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCCTTAGTGATTTAAGACTG

TIGR- A004Z19	85 C T	GAGAACACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGAGACAAGTTATTGGAGGAGCTTGACACCCCTCTTCTGCCCTAGCTTGAGAGACAACACTGC AGCATTTTTTCTTTTCTTCTCCGATGACCATCTTTTGGCTGGGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAAGGAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGAGGT AGGAGACT	CAGGCTGCGG GTCC	GTCTTAGCAGAGGATAACTTTGAGGGACAGCCCCCAAGGGCCAGGTAGCCTTCAGGGGCGGCA GGTTGGGGAGGTAGGAGACTCTGGACCCGAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGCTCTC
TIGR- A005D17 c	81 T C	GGGAAACCC AGCAAG	---	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCTCTGTCTAGATCTCTTGGCCCTCTGTGCGAGGATCTCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D17 b	79 G C	GGGAAACCC AGCAAG	GAGAGGCCAA GAAGAACTTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAG[G]CTGTCTAGATCTCTTGGCCCTCTGTGCGAGGATCTCTCTTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAAC
TIGR- A005D44	97 G T	TTAACATTAT GAACCTTAAA CTGTTACAC	TTGCTATTAT TTAAAGCCAAC AAAA	CATCAGTAACATATACACAATTTGGTCATCAACTGAACCTTGCCCTCCAATATATTTCTATACAATCTT AACATTATTGAACCTTAAACCTGTACACTG[G]TTTTTTGGCTTTAAATAATAGACAATGATTTTTTG TCTATTACTTAGTGATAGACAAGAGTGATTACTTTGTTAGACAAAGTGATTACTTTGTTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAATTTATAACCAAGGCTCT[G]AJCTCACAGCTGTACTGGCTAGGCAAGCTTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTTGCCTGCTTGCCCTTACAAAGCCACTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	---	---	CTCAGTGTAACAACTTTGTTAGGGAAAAAATAATCCAAATGGATATATGGGAAGAGAAGTG CCAGCTGGATGGTGTGAGACAGAAATGACCCCTTGGCTCTTTATTTGTTCTTTTCAACAGGACC CCACAGATATTGCGGTATGTCATGAGGACTGGGATGCTCTTATG[C]GGATGCTTCTATT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTGTATCTTAGTAAGGTACTGCACCTTACAGAG/GTCTCAATTTCCCTGATTTAGGA AGCGGATGCTAATGGGTATTGCATAGGTGAAGTATAAAAATGTTGATTTTAAGAGAAATCCCACAAG CTTGGTATAAGGCAGAAAAATAATGGTATAAGGCAGAAAAATAAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGTAAAGCACCTACTGCGTATCAGGCACCTGACTCGG TGCTTTAC[G]ATACATTACCTCACAGCCAGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTG ACAC
120979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA[C]TGCTTAGGGTGTCTCCCCACAGAGCAGATACTTTGAACCG ACTCAATTCCTGTGTAAGAGCACTTTGTCTGCTTACGGACCTCCCAAGGTGTCAGAGTTCTAT ATAGGATGCTGGATTAGTTCCTTTGATATTTGTAAAAATTCGCCCAAGAGCCGCATATGAATCTGCCC

X57830	106 G C T	AGTGGAAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTGGAAAAAATAATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAACGATCATATCTG/CJATGCTCATTTTATTCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGTGCTTGGAAAATGTTCTGACAGCATTTTCAGCTGTGAG CTTTC
X74070b	72 T G TGGATC	CTTTTAAAGAA ATTTTGTGTTA	GGGCTTAAAAA TATTAGAGATC TAGATTT	AACCTGAAGAAGTTACTGGAGCTGCTATTTATATTAGCTGCTTTTAAAGAAATTTTGTATTAG GATC/T/GJGATAAATCTAGATCTCTAATATTTTAAAGCCCAAGCCCCCTGGACACTGCAGCTCTTTT CAGTTTTTGTCTTATACACAATTTCATTTTGCAGCTAATTAAGCCGAAGAAGCCTGGGAATCAAGTTT GAA
Z48804	44 C T ---		---	ACTGCCGAAGTGTAGCGGCCCCCAAACTTGTCTCATCACCAG/C/JTAGAGCTTCTCCCGAAGGG CCTTAGGATAGGAGAAAGGTTTCATGCACACACGTGTGAGAA TGAAGAGCCCTCCAGACCACT CTACAGCTGCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGTAAAGG TCCA
D28513b	133 A G ---		---	ATGACCAAGCCACCACATTTAGAACTTTGGCTGCCCTTGGAAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTCAGCACCTTTGGACATGGCTCACAAGCAGTTTTTATTGACTGCATGAATGC/J G/JGTGCGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85 A G ---		---	CCACTCCATCTCTGATGCCCCAAGTTATCCACAGCCTCTTCCCGACCAAGACCCTATCCACCTGGACC TCCATTTTCCCTGTAA/JGTCTCCAAGTATCCCTACCTCCCTACCTCTGACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCACCAAAAGACACCACTACCTTGTAACTACTGCTTCTGCTAC
D29833a	21 A G ---		---	CTCCCTGCCTCCTCCTCTGCTGCCTGTGATGCTCCGCTCAAAACAGCCGAAACCTGTCTTGAATGGGGG GAGGGGGGCTTCTG/JCTTCTCTCTTGGCTTCTCTTATCTTCCACAAACCACTTCTCAATAAA GCCAAAAATCTTCTCTTCTCCCTCAGGCCACCTCCTGTGCTCACTCTGTCTGTGCTGGCTTTT CTGGA
D31762	82 G A ---		---	ATTATCGGAGTGGTTGACCTTACACTTACTCTTAATAGCAGTGAGTAATGCATTTTGAGCTG/JCJ CCCAGGCTCTGTCTCCTCAGCTCATTTCTCTACTCTTTTCTCTATATACTCATCTTATTAAATACATT GCACCAAGAGATATGGAGACATAAACCTGTATGAATGAGGCTGGGCTTTTCTGTAAATAAGCTTCC TTT
D37931	64 T C ---		---	

D63807	101 C T ---	---	---	CAGGACGGACTTCAGTGTAGTATCCCTGGCTTCAGTCTTCTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGAGTGATTTTCTCTGTTCCAC/C/TGAAGAGGACTTTTGTTCACAATTTGGATCAC AATGCAGAGGAGTCTGTTCTCTCCCGCTCGGCTTCCTCGGTGGGAGGTGACCTGTCCCAGATGAC
D90145	21 T C ---	---	---	TGGAAACATGGGTGTGACCTC/T/CJACAGCTACCTTCTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGGGACTCTTCTTAACCTAAATTTTAAATTTATTTATCTATTTAGTTTATATAATTTTATTTGAT TTACAGTGTGTTGTGATTGTTGCTCTGAGAGTTCCCGCTGTCCCGCTCCCGCTCCCGCTCCCGCTGAGTGTG TCTGGTG
EST14035 1a	59 T C ---	---	---	ATTATCACTCTCAAAAATTTGGTGTGTGTGTTAAGTACTTCTTATTTATGAGCCCC/T/CJGAGGA CCAGACATGTTATTATCAAGCCCCCTATATACCATCTAAT
EST16668 5	71 C T ---	---	---	GCATTTTAAATTCACATTTGAATCATTATTTACTATTTATGATGTTTACATAACAATTCAGTATCATT ATG/C/TJGTAGATTCAGATGTAGTGTCTCAATACTGAGCATTATCT
EST16904 7	57 C T ---	---	---	ACAGACTATCGCCAACCTTATAATGCTTAAACCTTTATGATCAATAGTAATAAATTACA/C/TJGAGATA TTCACACTTTATTATAAATAGGGTTTGTGTAAGATGATTTTCCCACTGTAGGTTAAT
EST21863 9	49 A G ---	---	---	TTTTAAGTACCAGAGGCACTGTCTGGAACAGGATGAAACTGATACACCC/A/GJTTACTACTTACTC TTCACCTTTCAACTGATTCCTTAAAGACTTCTACTTAGCAAA
EST21885 6	80 G A ---	---	---	GGCTGTAAGTAGAATCAAGGTTAAGAACATTTTATGCACTTATCCACAACACATTTACTGAGCATA CTAGGTGCTGGG/A/GJGTGACAGTGAGCAAAAAACACAA
EST22623 8a	26 A G ---	---	---	ATTTTAGTGCAAATGACAAAGCCCAA/A/GJAGAACAGAGGATCAATAAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTTAAACAAAGTATGGAGT
EST22644 2	98 A G ---	---	---	AAAATGATTGAATTCAGCAAGTACATTTTATGATCTATCTACATTTGTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTTACAG/A/GJAAATGTGGAAGATGGCTTTTAAACCC
EST23587 1	31 T A ---	---	---	CCTCATTTATTTAAAAAGACGGACATAAAAAA/T/AJATACAACAAAAACCCCAAGTCACATTTTCAG GAGTAAAAACTAAAAAGTCTGATATGAAAAATATGGTGG
EST24246 7	106 T C ---	---	---	AAAGATCTGGCATTATTCACATCATCTAAATATTTTGTAAATTTTCTCCATGAGTATTTTTC TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACCT/CJGAATAACCCATAGTTACAGAATTGG GTCTGTGAACCTCAAT
EST24308 3	45 A G ---	---	---	TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT/A/GJCATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAATATAAACCTCGTTC
EST24435 6	73 G A ---	---	---	CTTGAACCTCTGGTCTCAAGTGGTACGTCGCTCAACCTCCCAAAATGATCGATTACAGGCATAAG CAGCC/GJATGCTGACCCACATTTCTTTATCCGATCTGTGATGGACATTCAGGTTGTTTC
EST25089 6	25 T C ---	---	---	TATTGTTGCATTATCAAAATGGTTAT/CJAGTTTTCAATTAACACTGTAATTTCTATGTATAAA ACAGCTTGAAGTTGTAATGTAGTTTCCCAATCGTTAGTTAATGCTACATT

EST25476 9	33 GA ---	---	---	AATGATCTTTATTTTCAGACCTGCTCCTAAA[G/A]CTTTCTCCTCCTCTAAACCAACACACA AGAGGTCTCTTGCTGCCCTTCCATGGAGCTGGCGGCTGTGGACTGGACCGTCTGCTGA
EST26183 2	70 TA ---	---	---	AGATAATGCATTAGAGCCTGCCCTCATTGTATCTTGATTAACTTTGTAAAGATTGATCTCTAAATAAG ATT[A]ACATCTCTGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28 TC ---	---	---	AGAAAATAAGGTGCTACCAAGAACTCATG[T/C]GATAGCGCTTCTTTTAGGCACATATTATAGCATT CAGATGAAAGTTCTGTAAATCACACACACACTGTGCCCTAACAAACACACGGTGACTCTGA
EST27816 5a	26 TC ---	---	---	CAACTCAAGGTACAAAGACAATTGCATT[C]TAACATTGTTATAATAAAAGGAACATCAGATCAAT CATTAAAGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST28588 0	78 AT ---	---	---	GTTTAATTGGCGTATGGTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGAGGTCTCAGGAA ACTTACAATCA[A/T]GGTAGAAGGCAAAAGAGAGAGGAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGGAT
EST30226 5	25 AC ---	---	---	TACTCACACCGACATACATATCTCA[A/C]GTAGAATTAGTATAGTACTGCATACTAACTTCATTGTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGCTAACTTAAACAAGACAGACTCAATTCCTTTGA G
EST30935 9a	59 CG ---	---	---	AGCTATGGTAGAGCAAAATCCAGTGGTAAATCAAGAACTCTAAAGTTTCAGTAGAGA[C/G]AGGT GTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGAGG
EST32515 7	25 GA ---	---	---	CCGAATATAAGGAAAAAATGGTGG[G/A]TGCCCTCTAAACCTGTTGAATAGAAATATGGCCAAAT ATTACAGTTCTCACCTTCCATATGAATACTGGCACTGTTATTTCATGTTTATATGTAGATTCTATGC ATAAAAATCCAGTAAGA
EST33274 4	27 TC ---	---	---	TGCTTTGTTCCCTCCAAATCCATAAAAT[C/G]GTGTGTCTTCAAAGAAATTCGTGGAAGGACTTTGAA TACGAGTTTGTACCATATTCGAATATTCGAATACAGGTTTCAGATAACTATGGAGATGATACCAT GGACTAGGTA
EST33352 7b	75 CG ---	---	---	TACACATTATTCAGAGACCACCTGACATGCATCTCCTCCGAGAATACATTCGTCTCTCTAGAGA AGTTTA[A/C/G]GCACATAGTATTATTTACTAAGAGAATATCTCTTGGTGTCATATCTAGGGG
EST33424 1	126 AC ---	---	---	ATTTTCCACAGCAGAAGTATTTATTGTGCTGAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACAGTACAGAATGTTCAACAAAGATTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAA CAAAGGTGTGAATCCTCTT
EST33488 7	90 AG ---	---	---	CCTTTGGGGGAGTTTAAAGCCAGAATGTGACAAAAGTCACTTACAGGAAGACTGGGAATGTAGCCATAG TTGAACCTTAACATCGTCTATAG[A/G]ACCATTTCCTCGTCTCCAGTTAGGTTCTAGGCATATAAGCT GCTC
EST33508 1b	45 CT ---	---	---	AAAAACATGCTATTTGAACAAAACCTTTTATAAAGAATAAGTTGA[C/T]TGAAAAGCAGTTTTAAAT AACATCAACTCACAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36	A G	---	---	AAAAACATGCTATTGAACAAACTTTTTTATAAGA/A/GJTAAGTTGACTGAAAAGCAGTITTTAAAT AACATCAACTCACAATGACTTTTAGAAGCCAAATAA
EST33863 4	77	C T	---	---	ACAACATAGGACTGGTTATCTTGTTTTGAAAAATTATGTGCCACTTCCTATTGTTTTAAAAATGA TCATTAAAC/C/JJCTTTGAACTACAGCCTGAATCCCC
EST34739 3	97	T A	---	---	GAAGTATCCTCCAGTGGCAGGAACCTGAAGACTCCAGATCAACACAGGTGGACCTTTTCGTGATGA GCTGATAGCTTAGGCTGGGGAACCTC/J/AGGTGCCCTTACAACCTCCAACACTACTGCAGAAATTTCT TGTTGGCTCATAAACA
EST34792 6b	104	A G	---	---	ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCAGATCAGTGCGATCCACTATCAATA CTCATAAGCTTAATTTATCCTCAGGATGTTCCCTGA/A/GJGATTCAGGAATTCCTAGTCTATTACA AAGATTTGTTGCTGTG
EST34835 9b	93	T G	---	---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGCTATGTTGTGCTTCTGGT/G/GGCCCTTAAAGAAACAGACAAAATTTGTGCTAAAGAT
EST34835 9a	82	G A	---	---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGGAGCTATGTTG/J/AGTCTTCTGGTGGCCTTAAAGAAACAGACAAAATTTGTGCTAAAGAT
EST35230 0	93	G T	---	---	CACAAAGTCCACTTACTACATGAAGGAACATAAAGGCATGAGAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAGAGGTTCTC/G/JGCCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33	C T	---	---	TCCTTTCAAAATTTTGATGAGGCATTTAATG/C/JTATAAAATTCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAAGTTGGGCATGTTGTGTTCCATTTTACTAGTTCAGAACTTTTCAATTTTCATCT
EST35708 9	32	C T	---	---	CTGCCCCAAATTAACCTTTAGGCAATGGAA/C/JTAGACTTACTGTATGGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTTCCCTCTCTGAGGTTGGCACCTTTCTGTTGTG ATGTGCAAGTGTGGCT
EST35747 9	51	C G	---	---	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCACAAGGCTCCA/C/JATGTTAAACCGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCTCCAGTAGGGTTGAGATT G
EST35751 9	89	C A	---	---	TGGTCCATTATATAAACTGAGGGAAACAAACGGTGTGACATGGCAGACATTTATTCAATGGAGA AGTTCCTCCCATGAACCAAGA/C/JCTTGCTCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATATAATTAAAGGCTGTGA
EST36301 4	93	C T	---	---	CACCTGTTCAATGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTCTAGCCTACAGC AGTCAGGAGGCGCCATGGCCCCCTG/C/JGCTGATGGAGCTGTAAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33	G T	---	---	GCCATCAGCCCCACAAGACATGACTACCAACG/C/JGGCCCCCTTGACCCCATCTAGCCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGGCTTAGTGTG

EST36620 6	50 G A ---	---	GACITTTATTAGATAAGGGGTTTCGGCTACCCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAAGG AAGGCTTATTTAAATATGGGAAATAAAATACAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 C G ---	---	CCTGTGATGTCATGGTGCCTGAGCAGTCGTACTTACTATGCTGACAGACGCTACGTCATGTCAGGA AAGGAAGTCTGGGGATTCTA[C/G]AGGGGACATATCACACATATTCTAAGTCACCTGTGTGACTCGG CTTGAGCAAGTCATTTCA
EST36729 9	62 C T ---	---	GAGACAGAGCCCATCAGTTAAATGAGGTTAGGCCTCTCCTCTAATATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACCTTAGCTACCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 A T ---	---	ACTGTCTGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATT[A/T]TCTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---	---	ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTTACAACCTGACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88 T C ---	---	GGTCTACTCTCTTGCCAGGACGGTTTGAAACTCCTGAGCTCAAGTGACOCCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACCACACCTGGTCTTGTTTAAAGTAACCACTGAA C
EST37269 3b	105 T G ---	---	AATAGTCTATGGCTACGGGCCCCGTGGGATGTTAAAAATTTGGGATTTTAAATTAAAGATTGTGAACATG CAACCCAGCAAAATTTCTCAGCTTATATTTTGAAGTCT[G/C]AGGAGAAAAAATGGGGTCC
EST37284 2	93 G T ---	---	AAAAGACCTTTCTAAGCAGTAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAAGGAA GCTCTCTGGATAATGTCACTCTAGGA[G/T]AGTAAACAGGTGTTAAACCCCTGAGATAGCAACCCCT CTTGGCTTGTGAGGAATA
EST37315 2a	90 A G ---	---	AGATGGGGTCTTGTAGCTTGCTCGGGCTGAACCTAAAGATATCCTCCTCAGCCTCCAGGTAGT TGGAACCTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTGTGATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACCTT[C/T]AAGGGTGAAAAAGCATACC ATTCCATTTAGTTGAAATATTCCTTCACATAGCCAAACACATTTTTTCAAGGCACTCTAGCTACTACA GGA
EST37376 8b	101 G C ---	---	GTGACATCATGTCTCTTCAATGCCCTTTCAATTAAATAGTAGT[C/T]GAGCGCTGGGGGCTGAAGTCAGACT CTCTGGTTCAAAATCACAGTGTCTGTCTGCA[G/C]GCTGTCTCAGGCAAGTTGCTGACTTCTCTG TGTCACGG
EST37376 8a	41 T C ---	---	GTGACATCATGTCTCTTCAATGCCCTTTCAATTAAATAGTAGT[C/T]GAGCGCTGGGGGCTGAAGTCAG ACTCTCTGGTTCAAAATCACAGTGTCTGTCTCTGAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG

EST37378 9	63	T G	---		ACACACAAAAAATGGTGGCAGAAAAATCTGGAAAGATTCTAATAACCTCAATTCGTGAAAAAC/T/G JAACATGCCTCAAAAAAGAGGGGAAAAAACTTTAAACAGAAACACTGTGCTGACATTAGCTT
EST37452 4	46	G A	---		AAGACATAATCTGCAATGAATCAGTTATGAAATATTAAACCTCT/GA/CTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAAATCAATGACGTAGAA
EST37613 6	34	A G	---		CTAGGCATGGGCTTTTACAGTCATTTATTTACG/G/G/CTCATGAATTCATTAACAAACACAGCGAT ATAGCAATGAGCAAAACAGACCTCCCCAAAATCACCTCGGTCATGGATCTTCCATTCTAA
EST38025 4	56	T G	---		TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTATATCACATT/G/TTATCTCA ACAATCTTGAAGGGTGGTATTATTTCCCGTCTTATAGGTGAAGACCTGAGGTTTCAGAA
EST38068 6	57	C T	---		TCTACAGGTCACCAAGTATCTGATATGCTTTAAGTGGCATTTTCATGTACATT/C/TTJCGCATGG AAGAACGCTCTCTTTTAAATCCCTAACTCTCTTCTTCTGGGAAGACAGAACGTGCACAA
EST38420 6a	100	T C	---		TAAATCAAGGCCTCTTTTCAATACCAAAACAAACAAAAAAGGGAACAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGCATCTGACTGAC/T/C/CTCCCTGCAGTGCCCATGGGTCCCGTGCCT TATTCATTCTCTCTCA
EST38950 5	25	T C	---		TTTATTGCAAAAGTAAGCAGCCGG/T/C/JTGGTCCCTGGATTGAGGCTGAGGAAGACATTACTTCTCTG CTGGAATACCTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGGAAACAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90	T C	---		TTTTTTGTTACTCTGTAGCCAGTCATTAAATCTGAAGTTTAAATATATCATTTTATTTGGGATGAGATCA TAGCTTTACACAAATGCTATG/T/CAACAAAGTTACTGAATATTTTTCACCTCGTGGAGTTG
EST39331 1	70	G C	---		TCCTCTTGCTCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAGACCAGCCCATGGAAGGAAAGTA TGC/G/CTGTTTGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGACCCAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31	C A	---		GTCAACATTGACCTTACATAGTGCCCTCTAGT/C/AJACCTATGAGGCCTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37	T C	---		TTCTAATAGCATGCCCTGTGACAGGGAAACTAAGCTC/T/C/JTCAAAATAACTGAAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCTTTTGTAGTTTCTCCAGAAGGCTCAAGGTGTTT AATAATCTGTTGGACTCA
EST40549 1	42	A G	---		TGTTTCTCTAGAGAACCTCTGTGATACACTACGATGCACA/GJATAAAGTCACATCAAGACTAA TAATCTAAATGTTAGTTTGTACCACCATTTCTCACTTTTGAACCTAGTCCCTGCAAAAGCACCTTCTA CCCTGCACTTTTGGGAG
EST40579 1	81	A C	---		TGTGAATTACACATCAGTAAGGCAGTTTACAGAAATTTTCACTTACCTAAAGTCTGTGCTATCTG AGCTGGTGGAAA/A/CJGGACTTGGAGACAGCGATTAAATACGGAACAGGTTCTTCCAGGAAG
EST40584 3	68	A/G	---		TTGTATGGTTGAGGAATTTGGGAAGAAATATCTGTGAAGGAAATTTGCCACTGTGAATGCACACCC A/A/G/TTGTACTCCCAATATCTATGTTTAAAGCT

EST51340	51	G A ---	---	GATCAACTGTATTGCCAGGCCAGCTCCTGAAGAAGTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTCAAACCTAAGAGCCTCTCTAAGCTA GATAGCCCAAGGATTATT
J04162	134	T C ---	---	CATGGGAGTAATAAGAGCAGTGGCAGCAGCATCTGAAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAAACATAGAACTCAGAGCCAGATCCTTTATCCAACCTCTCGA TTCJTTCCTTGGTCTCCAGTGAAGGGGAAAGCCCATGATCTTCAAGCAGGGAAGCCCCCAGTGAGT AGCTG
K01506	63	T C ---	---	CTGAACCTCAGCTGCCCTACAAACTCCATCTCAGCTTTCTCTCAGCTTCATGTGAAAACCTAC[T/C]C CAGTGGCTGACTGAATTGCTGACCCCTCAAGCTCTGTCTTATCCATTACCTCAAAGCAGTCATTCT TAGTAAAGTTTCCAAACAATAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTTC ATTGAGCCCTTTATCCT
L18877	69	T C ---	---	TGAGTCTGAGCACGAGTTGCAGCCAGGCCAGTGGAGGGAGTCTGGGCCAGTGCACCTTCCAAGGCC CT/CJATCCATTAGTTCCACTGCCCTCGTGTGACATGAGGCCCATCTTCACCTCTTGAAGAGAGCAG TCAGTATTGTTAGTAGTGAGTTTCTGTCTATTGGATGACTTTGAGATTTATCTTTGTTTCTGTTGGA ATTGTTCAAAATGTT
L31848	36	T C ---	---	GCTATTTACATATCCCAAGCCCTTAGGGCTACAG[T/C]CTCTTGTCTGACCCCTGTAGGGTGCCA TTTGGAGTTCACAGCCTAGAAGAAGAAAGGCTTTGGCCCTGGTGTGGTGCCATAGGCCCTGTAATCGT AGCGCTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTCGAGACAAACCTGGGCAAT GT
L38517	137	G C ---	---	GGGTCCAGAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATAGACTTGACTGGGCAACACCGCTCCGCCAC CC[G/C]CGTGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTGACCCCTCT CTCTAGAGACCTTGAG
L39059	123	T G ---	---	ACTTGAGAAGCAGAGCTCGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGGCAACAAAATACAGTAGTCTTTCTTTGTATTTTGTATATTTG/JGCGCTGA AGATCATCCCGCAAGGCAGGCTGGAGGTGCCGTGGCCCTGTGTCTGGGATTTAGTCTGTGCTGG GAG
L41268d	173	G A ---	---	CAAAGTTGTCTCTGCCATGAGCACACACAGTCAGGCCCTTAGGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGCCGTGAGTCTGCAT CTTAGGGCATCGCTCTCTCTCACACCACAAATCTGAAC[G/A]TGCCTCTCCCTTCTTACAAATGTCT AAGGT

L48728b	111 T C ---	---	---	AAGTGAACAGAAAGCAAGATGGATTGTTCTCTATAAAAGCACATAGTATGTTTACTGGTATCGT AAGAAAGCTGGAAAGAGAGCTCAAGTTTTTGTTTACTTTTCTCAGAAATTCGAAAGAACTTATTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAACATCATCCTGTACCTTGGAGATCCA GTC
M18079	52 G A ---	---	---	GGCACAGTCCAAAATACAAATGGACAGAAGATCTATATTGTACAGAACTTCG/AJTATTTTCACC CCATCAAGTATAAGGTTACTGATTGATGGTCTTTTATAAACATTTGGTATATTTCCATTCATGGCAA AGCAAAAGAAAGTAAAGCTAA
M19169	113 T C ---	---	---	TAGGGATCTGTCCAGGCCATTGGCACAGCCACACCCACTCCACCCCTGTAGTCTCCACCCC TGGACTGGTGGCCCCCACCCTGGGGAGGCCCTCCCATGTGCCTGTCG/GCCAAAGAGACAGACAGAG AAGGCTGCAGGAGTCTTTGTTGCTCAGCAGGGGCTCCGCCCTCCCTCTCGCTTCTAATA GC
M21539	114 T G ---	---	---	TCACCTCGTTCACAGCTCCACCTGCATCTTCTCATCAAAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCCTTAGCCTGTGATCTGCCCATGATATCCCGACAGCAAAATG/GTTCCTTTCTGAGGCTG CCATGTCGCACTGTCCAGGTGGAGACTGAGCAAGGAAGTCTCAGCTGTACCGGCCCTTCAGAGCT TCCTTTGGGTGC
M26041c	173 A G ---	---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAAATGTTTCTCTCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTGAATTAATTCCTGACTTC CTGATTTTCTCTTCTCAAGTGTACCTACTAAG/GATGCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157 A G ---	---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAAATGTTTCTCTCTCACCTCT TCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTGAATTAATTCCTGACTTC CTGATTTTCTCTTCTCA/GGTGTTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45 C G ---	---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAAATGTTTCTCTCTCACCC TCTCTGTGGGACTTAAATGCTATATCTGCTCAGAGCTCACAATGCCCTTGAATTAATTCCTGAC TTCTGATTTTCTCTTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57 G C ---	---	---	TAAGGAGCTGTCAAGGAGGCCAGTCACAGTCCAGCAATTCACAACCCACTTGAC/GC/AATGCT TGCCAAAGCTGTTTAAAGCCCAAGAACACCCCTTCTTTGTTCCAAATTAACCTTAGAAGAAACCCCA CAATTAAGCAATTCATC
M81695	34 G A ---	---	---	ACTTACTTACCCTCACCTGTCAAGGCTGACGGGA/GA/GAACCACTGCACCACCCAGAGAGGCTGGG ATGGGCTGCTTCTGCTTTGGGAGAAACGTCCTGCTGGGAGGGGCTTGTCTGTCAAGGTT CAACTGGAAACCCCTTAGGACAGGGTCCCTGCTGTGTTCCCAAAAGGACTTGACTTGCAATTTCTACC T

U06641d	166	C T ---	---	---	CTCCTCCTTTATTTAGCATGGAGGGTTTAAATGGAGGATCTCCTTTCTGTGACAAAACATCTTTC ACAACTTACCTTGTTAAGACAATTTAAAAAGATCTTTTACAACTTACCTTTGTTAAGACAAAAT TATTTCCAGGCTATTTAATACGTACTTAC[C/T]JGGAAATTTATCTATGTCAATGATTTTAAAGCTA TGAATAACAATGGGGGA
U09607	39	T C ---	---	---	GAGGCCTTATGAGGTCCTCTACTTCAGGAACACCCCATTCGACATTCGATTTGGGGGGCTCCCG TGGCCTGTAGAATAGCCTGTGGCCTTTGCAATTTGTTAAGTTCAAGACAGATGGCATATGTGTCAG TGGGGCTCTCTGAGTCTCTGGCCCAAGAACCAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82	T C ---	---	---	GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGAAGCGTTGATTCCTCAAGGCCTCATCTGGAGCCTC GGGAAAGTCTGGTCTCTACATCTGCCCGCCTTCCAGCCCTTCCCGAGCCCTCCTCTTGTCTTCTTC ATTCAATCAACAAAATTTGGC
U10694	20	C G ---	---	---	GTGACATGAGGCCCATCTTCGCTCTGTGTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCATCTCTGGTCTCTGTCTATTTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAAAATGTTCTTTAATGGTCAGTTTAAATGAACCTTACCACATCGAAGTTAA TGAATGACAGTA
U13877b	162	T C ---	---	---	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGTCTATCTTTGTACCTTGCACAAAGTTGTTTAAAC CTCTTTGTTTCAAGAAATTTCTCCATGGAGTAACAATATCTAGGTGGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGGAACAGCCAGAGATTC[C/T]TACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTTACCTTCAGCA
U15555	187	T C ---	---	---	TTTCTGCCACTTTCACCTGGTTTAAATAGCCAGCCAGTCAATAATAGTAGGGAATCAGTCAAGCAA AAATGCTTTGGAAAGATTAAATAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGATCCACGACCCCTTTCTAAGCAGTCTGGTCCATGTC[C/T]TGGTCTCATAC CTCATATGCAGGATTCATTCA
U17077	122	T C ---	---	---	TCCAATTTATGGTCCCAAAAGCAGCTTCCAACGTTTGGCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGGATTAAAGAACGTCCTTGACAGCTGAGCGATGACACACACATTC[C/T]TGTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTCTTTTCTCTGGGAAAACAACTGTCTCTTGG AATTA
U18543	58	T C ---	---	---	GCACATGCAGAATAGACTCAGCCTATGTCCTGATTCAGCTGGGTAGTTCTAGAACTTTTCJAGAAG CTCCATCTTTTAAATGTTTTTATTTGTTATGTCCCCCTCCCGGCTTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAAATAGGACACAGATGGTGTAGCTGAAGTTTGATTAGCAATTAGGCACTTCC AAGCCTTTAGTAGAGAGGCC

U25975b	164 C A ---	---	---	TCACTGCTGGCCCTCATACCTCTTTTCCATTTTCTACAAGAAGCCCTTTTAGTATATGAAATATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAAATTGCAAAAAGAC/AJ/AGATATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAGGAATTGTGGACTGA
U25975a	143 C G ---	---	---	TCACTGCTGTGGCCCTCATACCTCTTTTCCATTTTCTACAAGAAGCCCTTTTAGTATATGAAATATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAAC/CJ/GJ/AGAGAAAAATTGCAAAAAGACAAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAGGAATTGTGGACTGA
U25997	61 A G ---	---	---	CAGGGAGAGGTTATTCACAACCTCACCAAACTAGTATCATTTTAGGGGTGTTGACACACCA/A/GJTT TTGAGTGTACTGTCCCTGGTTGATTTTAAAGTAGTCTCTATTTCTATCCCTTTAAAGAAAATT GCATGAACTAGGCTTCTGTAATCAATATCCCAACATTCTGCAATGGCAGCATTCGCCAACCAAAA TCC
U28413	29 C T ---	---	---	ATTCCTGACAGCTAAATTAGCCCTAAATG/CJ/TJGGGTAATATTTTCTCATGTTTAAATGAGGTT AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTCTTCTGATCC CAGATGTTGTGGCCCTGGGAAGCCCTCATTTGCTACAGTACAAAGTACACAAAGTCGTTGACCTCAGTT G
U30884c	89 A G ---	---	---	TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGTT CTTCTATCCACGTTAGCCA/A/GJ/TGCTCTGATGAATCTATATGATCATAAGACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTGCCACACAGTTGAACACAAAGT GCTGTCA
U30884a	34 A G ---	---	---	TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGC/A/GJ/GTGTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATCCACGTTAGCCAATTTGTTCTTGATGAATCTATATGATCATAAGACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTGCCACACAGTTGAACACAAAGT GCTGTCA
U31216b	78 A G ---	---	---	GGGACAGCATATGTGGCACCCGCTCTCTGTGCAAGTGAAGACCAATGAGACGGCTGCAACCAACA GCCGTATCA/AJ/GJ/CCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCCTTACAACGTAGAGGAGGAGGAGGATGCCAGCCGATTGCGCTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70 G A ---	---	---	GGGACAGCATATGTGGCACCCGCTCTCTGTGCAAGTGAAGACCAATGAGACGGCTGCAACCAACA GCC/GJ/TGATCAAAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAAGACCCCTTACAACGTAGAGGAGGAGGAGGATGCCAGCCGATTGCGCTTAGCCCGCC TGGTAGCCCTTCCAT

U31416c	76 G A ---				AGTGGCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G]CCACAAATCTGGTGCCCTCTCTCTGCTTACAATGTCTAGGTCCCACTGCGCTGCT GGAAGAAACACACACTCCTTGTCTTAGCCACAGTTCTCCATTACCTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T ---				AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C]TTCCTCACGCGCACAAATCTGGTGCCCTCTCTCTGCTTACAATGTCTAGGTCCCACTGCGCTGCTG GAAAGAAACACACACTCCTTGTCTTAGCCACAGTTCTCCATTACCTTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T ---				ACGGGTACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCACTCACATTGTTCTCTCC AGACCGCAGG[C]TTCCTCCAGCCTCAGTTGCTGGAGCTGCACATGACTGCATCTGCTGCCAGG GCTCAAAGCAAGGCTTGTCTTCTATCTGGGGACGCTGCTCGAGAGAGGCCGCGCAGAAC ATGCCAGGTGTCC
U37690	54 A G ---				GACCACGCTGAAACCCACCCCGCTGTGCTGACCATGGGCCCTGAGCGTCTT[G]CCCCGAAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCTGGCCGCGAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGGCTTT
V00540	39 T C ---				TGAAACCGTTTCAACATGGAATGATCTGTATTGACTAA[C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCCTATAACCACCGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106 A T ---				TCAAGAAGGTGACTGCCCTTGTATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCATGTGGTTTTAA[A]TATCCATAAGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAAGACCCCTAGAATTTGGATTCTCTCTGTTTTTTCATGCTCTCCTT GTAACCCCTGAGATCATCAG
X52011b	148 C T ---				AGGAAGATCCCAACCGACCCCTTCTGGCCTAACTCTTTAGATTAGGTACATTACATTACATTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAGGAGACACATTACAAAGAAAGTTGCGAAATTCGG AAATCTGTTGTGCA[C]TGTCTCAAATGAAACGCGCTTTTCGGCTTTGGGCTTTTATTTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118 A C ---				AGGAAGATCCCAACCGACCCCTTCTGGCCTAACTCTTTAGATTAGGTACATTACATTACATTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAGGAGACACATTACAAAGAA[A]C]GTTTGGGAAAT GCGAAATCTGTTGTGACGCTCAAATGAAACGCGCTTTTCGGCTTTGGGCTTTTATTTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT

X54741	24	A G ---	---	CAGGCCACCTGTCTCTCTCCACAGJTGACACAGCTTCTGAGTCACCCCTCTGTCCAGCCAGCTCCT GCACAAATGGAATCCCGAGGCCCTCCAGGACTGGGCTTGCCAGGCTTGCCAAATAGCAAGGCCAG GGCACAGCTGGAGACGATCTTGTGGCAGGGCCTGGCCTTGCCCCAGCCCACTGGCCCCCTTCTCC AGCAAGCAGTGC
X54869	99	A G ---	---	AAGCATTTGCGTTTACAGTGCATCAGATACATTTTATATTTCTTAAATAGAAATATTATGATGCAT AAATCTGAAATGAAATATGTTATTTGCTCTAGJATACAAAAATTTAAATCAATATTGAAATAG GATGCACACAATTAATAAGTACAGACATCTAGCATTTGTGCGGCTCATTTTGTCAACATGGTA GCCGTGCTGACACCTCAGAACGACGAGGTGCTGGGCCCCGTTCTGCCGGAACCCCGGGAACCTCTC CTGCCGGAAGCGGACGGAGGATGGGCCCAACTTGGCCCTGCCACTTGACTTCACCAATCCCT TCCTGGAGACTTGAAACCTGGTCTCAGGAGCGGAAGGACTGTGAACCTTGTGGCCTGAAGAGCCAGA GAAATGTGAAGAAATGTGACAAAAGCCTTTAAGCGGTGTGCACACTTGATTGTATATAAGATAAT/GJT CATACTGGAGAAAACTCCAGAAAGTGTGACAAATGTGACAAAACATTTAAATTTCTCATACCTTA TTGCACAGGAAAGCATTATACCTTGAGAAAAATTTGTATAAAGAAATGGAAGTCATTAATATCTGCT CATATCTTAACATCAGCGAGTT
X78932	62	T G ---	---	CTCAACCCATAACCTCAACCACATCT/CJTATCCTCCACCCACATCCACACATCCACCTCCATCC CCAACCCATCCTCATCCCCAATACAGCCCCCAACCCAGCCCCAGACTAATCCACAGCCATCCCCAA CTCATCCTCATCCCCAATGCAGCCCCCAACCCAAACCCAGGGCCATCCCCAACCCATCCCCAAGCC AACTCAACACCATCC
X80026	25	T C ---	---	ACCCAACTCAAGTCCAGGCCCGAGGCATCTTCTGCCCTGCCCTTGTGGCCCATCCAGTCCAGG CGCCTGGAGCAAGTGTGCTAGCTACTTCTCTCTG/CJACATTTGAAAGACCCCTCCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCCCTCTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG ACCCCAACTCAAGTCCAGGCCCGAGGCAGJCTTCTCTGCCCTGCCCTTGTGGCCCATCCAGTCC AGGCGCCTGGAGCAAGTGTGCTAGCTACTTCTCTGCACTTTGAAAGACCCCTCCCACTCCTGGCCTCA CATTTCTGTGTGATCCCCCCTCTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG GGCACCCAGAGTGACCAAGTCCAGAGGGAGGGCGGCCGCTCGCGGTGTCGGTGTTCCTTTT CAGCCCCGAGAGGTCTGACCTGGGGCTTCTCCAAAGCTACTGCGCCACGCTCCCCGCCGCTCT CTTTTCTCCCAAGC/GJAAACCAATGGGCCCTTCACTCGCGTGCCCGTGGAGGCCGGGGGCTT CTTTCAGAGC
X80197a	28	A G ---	---	ACCACAGCCATGGTCTAAGGACATGGATCGGGTGCCCGGAGCGTGTGCACAGGGGACCCCTCTGCCCG CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCTT/GJGGG ATGCGCAGGAGGAGCCATCGGGTACTACGCAGCAACACTCACAACCTGTCCAGGCTGAGATAAATCCC GGGA
X80197b	99	G C ---	---	
X80197a	28	A G ---	---	
X85106	150	G A ---	---	
X87160	128	T G ---	---	

X87344	34	CT ---	---	CATCCCAAGGCACTGGTGTGACTCTGCTTCTGTC/TTACTGACCCAGAGCCTCTGCCTGTGCACCTGC AAGCTGTGTCTACTCAGGCCCCAAGGGGACTCTCTGTTCCATTCTCCCCACACAGACTGTCAAGAG AAGCATGACAAACAAATCATTTACCGACTTTAGTGCCTTTT
X87838	179	GT ---	---	GGTGGGCTGGTATCTCAGAAAGTGCCTGACACACTAACCAAGCTGAGTTTCTATGGGAACAATTGA AGTAAACTTTTGTCTGTCCTTTTGGTCGAGGAGTAACAATACAAATGGATTTTGGAGTGACTC AAGAAGTGAAGAAATGCACAAGAATGGATCACAAAGATGGAATTTA/GTTCAAACCCCTAGCCTTGCTT GTTAAAAATT
Z14138	81	AG ---	---	GTTCTGCTGCTCTACACAGGGGCCCTGTACAGTGAATGGTGCCATTTTCGAAGGAGCAGCAGTGTGA CCTCTGTGACCC/AGTTGAATGTGCTCCCAAGCGGCCCTGTGTGTTGACATGTGAAGCTATTGTAT ATGCACCAGGTCTCAAGGTTCTCATTTCTCAGGTGACGTGATTCTAAGGCAGGATTTGAGAGTTTCACA GAAGGAT
Z18859	191	AC ---	---	TAACTCTCACCATTCTCAGGTATAAGTTCTATAACAGGCTTGGAACTCTGGGTAATTTAAACACAGA AAATTATAGTCAATATACCATGACATGAAGAATGAATCCATTCTTTGGAGATGGAGTATACATGACT GCAACTGTATTTTCATACGTTCTTTTCAAAGTGGGATAGCTATTGCAGCTTAAAGAGC/AC/CAGGTTTC CAGTACTGGTTTTCCAA
Z23091	159	GA ---	---	AGAACTGAOCAGATGTGGCTCGGAGGGGAATCCAGACCCGCTGCTGTCTCTCCCTCCCTCCCTCC CACTCCTCCTCTCTCTCTCTCTCTCACTGCCACGCCCTCTCTTCCCTCCTCTCTCCCTCCCTCCG CTCTGTGCTCTTCAATCTCA/G/AGGCCCGCAACCCCTCCTCTCTCTGTCCCGCCGCTCTCTGGAAA CTGAGCTTGACGTTTG
11595b	125	AG ---	---	GTTGGCATTGTTAGTAAACTTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGTTTCTGCAAGGGCAGGTTTGAACCTGACCCCTAGTTGTCTCCAGGACCTA/AG/GCGGTGC TCACTCTACCTTGTCTTTGTGTTGAAGAGGTGGTTCCCATGACTGTTTAAAGTGAAGTGCCCATGG ATATCTACACCGTCACAGACTAGATTGTCTCAATGTCTTGGCTTGGCAG
11595	125	AG ---	---	GTTGGCATTGTTAGTAAACTTTCATAGGTGAAGAGGAGGATCAGTGAGATTAAGTTATTTTATCAAA GTGTGTTTCTGCAAGGGCAGGTTTGAACCTGACCCCTAGTTGTCTCCAGGACCTA/AG/GCGGTGC TCACTCTACCTTGTCTTTGTGTTGAAGAGGTGGTTCCCATGACTGTTTAAAGTGAAGTGCCCATGG ATATCTACACCGTCACAGACTAGATTGTCTCAATGTCTTGGCTTGGCAG
1241	131	GT ---	---	TATATCACATTAGTATGTCACTGCCATGGTAAGGACTTTTGATCACTAGGAAATAAGAACACTTTTGAA TGGTCTTGTCCCTTTCAATAAAAGAGTGACATGATTGAACATGTGTTTATAGATAAAGGGCAGCTT/GT JGCAGGAGGTGTTTAGGATGAAGAGAGAGAAGAGATTAAGGAAGATCAGGAAGAAAAGTAGCAATGGGA ATGAAAATAGGAGGCCCTGAGATCCACTGGATAATCTAAAAAACCAAGAGAAAAG

1282	130 C T ---	---	GTGCGATCACCACACTAGTCTAAATTTACAGATGTTTTTCATTACCCCTAAAGAAATCTTTGTACCCCATTA GCAATTTATCTCTCATTCCTGCCCTCACCCCGAGCCCTACTCTTTATCGCTATAGATTTGCCQ[C/T]ACT TGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTTCTTTCACTGAGAATA ATGTTTTCAAGGT
6810	68 C T ---	---	AGTATCACACATACTTAAATATATTAGATATACACAATAATAAAATCACTCCCTAGCTTGAAAACTTT A/C/TJAGAAGCATTTTTAAATTTTACAACACAAAAGCTCAACGAACCTACAAATAGTCTAGTAGTCTG TTTACGTGCCAAGGGATAAGGCTGAACATAAATTAACCCCTTTAAAAATGCTATGAACAAAGTACAA TTTTCTTTTJGAGTTCTGCAGAGCAATGACCCTAAGAAATATTTTTAAAGGC
6817	118 A C ---	---	CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTGCTTTTGTAAATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGCAGGGTAAC[A/C]JGTGGATACCCCTG TGTGCTCTACTGGCCTCCAAAGGCATTGAGGGGATCATCAAAAGATGTTGGACACCTTGTGTTCAAATC TTGGTTCAGGTGCGGCCTGTGCAGATCGGCTTTTGGTTGGTGTCTAG
6819b	212 C ---	---	CCATTTTATTTTCTCTAAATTTTAAATAGAGACTTTTAAATGGAACAATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAGCCCCGTCAGTAGT ACACATTTCTCTATGGTCCCTCAACAGTTTTGCATATACAAAATTTCTGCTATTTTGTCTTAGCAAA CAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
6819a	166 G T ---	---	CCATTTTATTTTCTCTAAATTTTAAATAGAGACTTTTAAATGGAACAATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAGCCCCGTCAGTAGT ACACATTTCTCTATGGTCCCTCAACAGTTTTG/TJCATATACAAAATTTTCTGCTATTTTGTCTTAGC AAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
681xx	39 A G ---	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATTJGJTATACTATGGCACCATTTGGGACA CAGATTATATATGTCAGACACCCAGCAATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCTATGGT TTAACAAGAAATGAACGCTTAGG
6972b	149 G T ---	---	AGGATTCCTCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCCCTGGACTCTTTTGTGTTGGTAAACTATTGATTATGC CACAATTCAGAGJG/TJCCCTGTTATTGGTCTATTTCAGAGATTCAACTCTTCTCGGTTTAGTCTTGGGA GAGTGTATGTGTCAGGAAT
6972a	122 A G ---	---	AGGATTCCTCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCTCCTCTGTACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCCCTGGACTCTTTTGTGTTGGTAAJGJCTATTGATTA TTGCCACAATTTTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTCTTCTCGGTTTAGTCTTGGGA GAGTGTATGTGTCAGGAAT

7598k	210 A C ---	---	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGCAG[A/C]
7598j	208 A T ---	---	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGC[A/T]GA
7598i	192 G T ---	---	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598h	144 C T ---	---	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTGATCC[C/T]ATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598g	142 C T ---	---	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTTTA ATATTGAT[C/T]CCATTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598f	120 A G ---	---	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCCGCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598e	83 C T ---	---	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCCGCTAA[C/T]CAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598d	77 C T ---	---	AAAGGTAATCAAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCC[C/T]GCTAACCCAGATTTTACCTTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACACCCCAAGCCA[A/G]AGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATAATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAATCAAAAGTCCCTCTATAAAATTATGATTTACAAAAGACAC[C/G]CCAAAGCCAAAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATAATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAATCAAAAGTCCCTCTATAAAATT[A/G]TGATTTACAAAAGACACCCCAAGCCAAAAGGAAC TCAATGAAATAAGCCGCTAACCCAGATTTACCTGGAGAAATGAAAATTATTTCTTGAGGATGCCCTT TTAATAATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACCTTTAATGAATGGGTAGTCTATCTTCTCAAGGTCCCAATA[A/T]CCTTGAGGTTCCCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACCTTTAATGAATGGGTAGTCT[A/C]TCTCAAGGTCCCAATAACCTTGAGGTTCCCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACCTTT[A/T]ATGAATGGGTAGTCTATCTTCTCAAGGTCCCAATAACCTTGAGGTTCCCT
8071	119 A G ---	---	AAATACAGAAATTTTATTTAGAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCAGGTGG AAAATGGGTTCCCAATAAAATGGAATTTTAGGGCAACAAAAGTCTAAAAGGCC[A/G]CAAAAAGAGA AATAGCACCACGTGCAATTTGAACAATGGCTAGTTACTTTGGCAATTTTGGCAATTTGTTAATCACTGAATC TGGGTTTTCTCTGAAATCCACACAGAGCATGCACACACAATTTTATCAT
8467b	93 C T ---	---	AAGGCTTTCCTCTAAACATCAGTCTTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACCTT TGACGCAAAATCCACTTTGCTGTAA[C/T]GGTCAATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGCAATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTACTG
8467a	70 A G ---	---	AAGGCTTTCCTCTAAACATCAGTCTTACGGAGAAACTGGGAAATCCTGGATATTTGGCTTATCACCTT TG[A/G]CGCAAAATCCACTTTGCTGTAAAGGTCAATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGCAATGCAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTACTG
8498	84 C T ---	---	AGGGTTTCAGGGTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAG[C/T]AATACCTTCAATTAATCGAAAAAGAAAAATTTGCTTTAAGGAAAAAAA AATCCAGTTTTAAGAACAAATTAACATTAGTCTTTAAATAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCCTCAATACAGAACCCAGGAATGTAATTTTCTTAACCTCAG

WI-18562	29	G A	---			CTAAGGAAAAATTTAATGATGGAATATC[G/A]ACAATAATTCAACATCATTTAAAAACAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTCTTACATT TAGCATTAAATCAGAAACGA
WI-18618	51	A C	---			ATAGCAGACTTTTAATCAATGCCAGAGACAAAGTGAGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAGTATAATTGTAACCCACAGTGCTCGCACAGTTG AC
WI-18683	22	C T	---			TAAGCTGTTTCAGGACTGGACTC[G/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAAATAAATTTCTCTCCCAAAGCCTGCCTGCAGT
WI-18520	75	G A	---			GACTTTGGTGATTAAATGCTTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTTT ACTACA[G/A]CCGGAGTGGTAAATACTACTACCTACTGCCAACAAACAGGGCATCCACTCTGTCTTCAA TGCTCTTCGGTGAGAC
WI-18563	94	A G	---			AAATAAGTTTATTGGCACACAGCCAAAGCCCACTGGATGACACATTGTCCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGGCTCACAAAGCCAAAGATATT
WI-18582b	69	T A	---			GTCTATTTCGAATTTAGCTAGACCCATTTCATCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC [T/A]GTGCCATAATTTAATCAGTGCCATATTGAAGACATTTGGATCGTTTCCCAG
WI-18723f	94	G A	---			AACCTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCCAA[G/A]TATAAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71	T C	---			AACCTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGT[C/A]ACAGGTACATAGGTAACCCAAAGT[A/G]TATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96	A G	---			TTTATTACAATAATTAGGTGGCACAATACTAACAAGCTTCTGA[G/A]ACAGGAGGTAACATTCTCA TAGACTTTTGCAACTCAGCCAGAAAGTAAACTCGAAATA
WI-18619	44	G A	---			TTATTCACAAAAAGTGATATTGCAGAGGGTCTGGGGCTGTACATGGGAGGGGCTTGGTGAGCTTIG TACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGAAGGGTATTTTTTAATAAAAAAATAA TGGAGCTACAACCCACCC
WI-18715	76	G A	---			GTAAATAAGTTTATTGGCACAGCCAGCTCGTTTCATTTCATATGCCATTGACATCTGCTGTGCCCT ACACAGCAGGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCCAAC CTTCTGTGGTCCCGTG
WI-18535	107	G A	---			AGAGTGGTCAAGAACACAGGCCGAATCCAGGCTCTATCATTACTAGTTTTCAGTTCTGGCAGGTGAC TTATCTCTCTCGAAGTTCAGTTTCTTCATAAGATGGAAGTAAAGTACCTACCTACCTCGTAAAA GTCTGATGAGGAAAAAGATTAACTAATAGATGCATAGCAGCTTAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAAAGGTGATGTCTACAGGACGACGAAG
D17525	107	C T	---			

DWU-133c	313	A G ---	---	TAATTGGCCACTGGCCTATTATTACAAAACAGAAATGCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAAGATTGAGATCATGAATGACTGACAGAAATATTTGTTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTCAGTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C ---	---	TAATTGGCCACTGGCCTATTATTACAAAACAGAAATGCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAAGATTGAGATCATGAATGACTGACAGAAATATTTGTTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTCAGTTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T ---	---	TAATTGGCCACTGGCCTATTATTACAAAACAGAAATGCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAAGATTGAGATCATGAATGACTGACAGAAATATTTGTTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTTAAATGAATATGTCAGTTTTTGAATTTAATAGTAACCTCC TTCCAAATTCAGTAAATGGTATCACTCGTTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T ---	---	ATGAGATCCTTTAAATCCTTCCATGAACGTTTGTGTGGTGGCACCTCTACGTCAACATGAAGTG TGTTCCCTCAGTGCATCTGGGAAGATTCTACC[C]/GACCAACAGTTCTCAGCTTCCATTTCGCC CCTCATTTATCCCTCAACCCCGACAGGTGTTTATACAGCTCAGCTTTTGTCTTTCTGAGGAG AAACAAATAGACCATAAAGGGAAAGGATTATGTTGGAATATAAAGAT
DWU-387	169	G T ---	---	GTGTATAAATGCAACTGTTGATTTCTCAACATGGCTCACAATTTCTATCCCAATCTTTCTGAA GATGAAGAGTTTAGTTTAAACTGCACCTGCCAACAAGTTCACCTCATATATAAAGCATTATTTTA CTCTTTGAGGTGAATATAATTATTTACAATG[G]/JAAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTCACCAAGTATCAAGTAAATACACAAATGAAGTGTCAATTATCAA
DWU-447b	172	--- ---	---	ATTTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAAGTGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAATTAATTAGTTTGATTAGAGCACAAGCTTAGCTAATCAA CCATTATTTTTCATTTTGTGTTCTAAGAGGATTGANAATCAGTTAGTTTAAATGCTTTCTGTTAG GCCTTTCTTTCTTACAATGAAGAGATGATTCTCTAGTTTATGGTTA
DWU-447	85	A G ---	---	ATTTTAGTGTCTTTGCGTTAAAAAATCATTGCAAAAGTATTCTGAAGTGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAA/GJATCACTGTAATTAATTAGTTTGATTAGAGCACAAGCTTAGCTAAT CAACCATATTTTTCATTTTGTGTTCTAAGAGGATTGANAATCAGTTAGTTTAAATGCTTTCTG TTAGGCCCTTCTTTCTTACAATGAAGAGATGATTCTCTAGTTTATGGTTA
DWU-476	63	C G ---	---	GTAAAAATTCAGTTTTCAGTTCCCTCTTTTGTGCTGCTTCTCAATAGCGTTTAAAGGTGAGC/GJAT AAATCAACTGTCCATCAGGTGAGGTGTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67 A T ---	---	---	TCATAAGGGCAGTATCTCTCTAGCTAGTGCCCATACAGAAAATTCTATCACCATACAAAATTTA[A/T]TGCAGTATTTATGTTTTAAAGCACAGGTGTACCGAAAAGTGTGAAAAGTCTGAATTTATGGGTT CTATGCATGCAATTTTGCCTAACCTAGAGAAAGAGTTTGATAAAATTTTACCAGCTTTGAAGATGGAT TAACTTTTGACTTTGAGCTTTAAACTTTTAA
DWU-512	131 A G ---	---	---	AAATCCAGGCATTTTGAATCTGTTTTTCATGATTTATAGAGGGTTTACACAAAAGTCCACTTATTTAA AGAGCTCCACAGTGAAGATGGAGAAGGTGAACCTGCTTTGAATATTCAGATGTGTTTGGTC[A/G] TGCGTATGGCAGTGAGCAGGTATGTTTGTCTTTTGTCTTGCACTGAAATTTAAATTTGCTATCAAGAGC AACTATGAACGGTTTTTATTCAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C ---	---	---	AACTGCATATAGATAAATTATCCAGGATGTGGCTCAATCTTTTCAGCTTGTTTCTTACTACTGTTTGTGA ATATACAGTTTTTGTAAACCATATGATTGA[A/C]AAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATCTTGTCTTTTCAAAATATAGTTGAACAAGATTTCCCTTAAAAATT CCACCAGGATTAATCTCTAAAAATCTAGTCTCTGATTTGC
DWU-59	94 C T ---	---	---	CATTTCTTTGTAAAGGTAATGGACTCACAAAGGGGAAGAAACATGCTGAGAATGGAAGTCTACCGG CCCTTTCTTTGTGAACGTCACTTGGC[C/T]GAGCCGTGTTCCAGGTGGCAGACTCGTTTTTG GTAGTTGTTTTAACTTCCAAGGTGTTTTACTTCTGATAGCCGGTGAATTTCCCTCTCTAGCAGACATG CCACACCGGGTAAGAGCTCTGAGTCTTAGTGGTTAAGC
EST11	68 C ---	---	---	CTTGATCATGGGTGGAAATTTTGTGATCTGGGCTTCATGGGATGCATAAAATTTTCCAGTTGGTAAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63 C T ---	---	---	CACACTGGCATCTAGGCCCTTGGCTGCAATTCAGAAAGGAGAGCCAGTCCCCCTCTCGGAGAA[C/T]G CTGGTTCCCCAGCCCCACACCGGCTTTGCACACACAGGCTGTTGAGGCGAGGAGGTGGGTAAGACGT AGCTGTAGACCCAAAGCAACCAAGCCCTGGGACCCCTGCGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGGTCAATCCCATCATTAGACAAGACACATCTACATAATAAAAAAGT
WI-18014	40 A G ---	---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA[A/G]GAATGAAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97 T A ---	---	---	TTCCAATGTAAAGAGTCAAGTACCAAGTTAACTTTAGAAATACAAAGAGAACAATGATAAAATCTG ATCACAGTGGAAAAATTTAATCTTTTCATAAA[T/A]CTGACAGGTCAAGTAAGTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ---	---	---	TTCCAATGTAAAGAGTCAAGTACCAAGTT[C]AAACTTCTAGAAATACAAAGAGAACAATGATAAAAT CTGATCACAGTGGAAAAATTTAATCTTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	---	TGTAAGGTGACTTCTATAAGCTTCTAAACTGTCAAACCTTCAATTTACTGAGATTATTTTCAGGCCAAT GTGTC[C/T]TTGTTGGTCTGAGATTGATTATCATGCTGGTGAAGTTAACCTGTCTCTGTTTCA

WI-18063	105	G A ---	---	AGGCTTTAAACTGATAACAAATTTGCCTTTAAATCACAATACAAAACCTGACACTTTCATTCCTCCTTC CCATGTTTCTGATTTTGATGTAACCTTAAATTTGTTGATTCCTTTAACAATATACTGTAGCTGCA
WI-18078	86	A T ---	---	AGTTGAAGATCAGAGAGGTTATGGTTGGTAGTACCTGAACTCAGATTCAAACCTGGTCCAGTGTG TTGTTTTTTCAGCATCAGATGTCCTCACTAGCCAAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90	T C ---	---	CCAAAGCTCACTCAGTATTTAAATCATCTGCTAATTTTCATCCTTTGTTAATTCATCAGACACTGTGGT TTTCATCTCTAGAAGTTTGACTTTCGCGGCTTTTATACCTTCCATATCTCAACTTGTAAAGC
WI-18119	38	T C ---	---	GCAATCTGTAACAGTTTGGTAGTGTATTACAGAGGATTCCTGTAATGGATTGGAGTGGAGTACTTAC CACTATTTCACTGCTCTGAATAGTTCATAACCAACTACTGACAACAGTTTAAATTTGGTTCTT
WI-18142	66	T G ---	---	TTCAAGATAATTACAAATTGGAAGGGGACCAATAATTCACATTTTAAATCGAAAAATACTATATAC T/GJCCCAATAAATCAGATAAATAAGCTTCAAAAAGCCTTAAAGACACCAAAAAGGAAAA
WI-18178	68	T C ---	---	GCATAGGTTGAGGGGTGTACAAGAGGAGAACCAAGATTCAGTCCATGCCCTGGAGGTTAGTCTGGGG GT/CJCGGCGGGATGGACACACAGACAGACACATAGATCTGGCATCTGATAGCAGGGCATACAG
WI-18244	35	G T ---	---	TCAATCTGAAACTTGTGTAGCCAGCATGGGTGTTGGGGAGGTGATTATGGCTGGGGAAGATG GGCACTCACCCGACAGCAGCATCTAGCACCAAGTACAGGGGAGCTTGGGTGGCAGAGGGCTTT
WI-18245	115	G A ---	---	ACAGATGTCAGTTGTTGATTGGCCCAATTAAGTATGGGCTTTCTGTTAAAAAGTCATCCAAA AGGCTTGGCAAGAGTTTGCTATACAAACGGAGGGACAGAGAAACATGA/GA/CTGGGGAGTAGGCTCT GACAGAAGGTGGGCTGTC
WI-18261	26	G A ---	---	GATTTGAAGGGATTGCTTTATTTAACTGATGAAAAGCGTGATAGAGGAACCTGTTAAGATAACAA CTTATAAATCTCCCAATTTGTAAGAGTGAAGATTG
WI-18268	88	C T ---	---	TAGGAGGGAAGAGGAGGTGGGCTGCCCTGGGCCCTCAAGACATGAGAACGGGTGGTGGCTTCCAAGC TTCTTACTTCCCCCATAGATTCCTGACAATGTGCTGCAGAACCTCCAACTGGAAC
WI-18299f	107	C A ---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTGCCAAATTTTTT ATCTATTTGGGCTGAGAAATCCACAATTTTGA/GA/CTTTTGGCAAATTTATGACATATCTG CAG
WI-18299g	101	A G ---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTGCCAAATTTTTT ATCTATTTG/GA/GTCTGAGAAATCCACAATTTTGAAGAATTTCTTTTGGCAAATTTATGACATATCTG CAG
WI-18299d	77	G A ---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTGCCAAATTTTTT T/GJATCTATTTGGGCTGAGAAATCCACAATTTTGAAGAATTTCTTTTGGCAAATTTATGACATATCTG CAG
WI-18299c	67	T G ---	---	TCACAAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTGGTTGCCAAATTTTTT T/GJATCTATTTGGGCTGAGAAATCCACAATTTTGAAGAATTTCTTTTGGCAAATTTATGACATATCTG CAG

WI-18299b	52	G A ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACATTG[G/A]TTTGCCAAATTTT TTATCTATTGGGTCTGAGAAATCCACAATTTGAAGAATCTTTTGCCAAATTTATTGACATATTCTG CAG
WI-18299a	48	C T ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACATTG[G/A]TTTGCCAAATTT TTATCTATTGGGTCTGAGAAATCCACAATTTGAAGAATCTTTTGCCAAATTTATTGACATATTCTG CAG
WI-18307	76	G A ---	---	TCAACTTGTAACCAAGTTTAGCAGCAAGAGGATACTTCTTAGAGACTTTTTCAGTGGACTTAAACTCAG TTCCCGCTG[G/A]TGCTATGTAAAGCATCCACGATGGTTTATTGTACTCTGCAATCTGCTTGGTCAC TTGGTATGAAATCTTCTCTGACATTTACCAATCATCACITTAACCTCCGGGGGGTGGGTACTGATT TATC[C/T]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18324	72	C T ---	---	ATGAAAGTCACCTCAATCATAGGGTCAAGAGAAAGAATGTTTCAGAT[C/G]TAAATCTATGAAAA GGTGTATCTGCTTGCAATTTAAGAAACAACACAAGTCA
WI-18350	48	T C ---	---	TCTTGACATGATCTGTGAAATAACGTGATTGTGGTTGAATTCCTGGAAAAATTTGAAGAATAAAATTG ATTATTCAG[G/C]JTGTCATTGGTTTATACATATCTCCTCTCTTAATGCAAGCTATG
WI-18395	77	G C ---	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG GATAACATTGCCAGTATAACCAATAATTCAAAACAAGCAGCAGAAATTTGGAGGATAATTTGTT
WI-18398	62	G T ---	---	CTCGTTGGTATTCTCTCATCC[C/A]TTCCTTTTCGCTCTTTCTAAATTAAGAAAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAACATTTAATCAACTTATCAACTTGTACAAAAGTC AATGAAAA
WI-18396	21	C A ---	---	AAGATGGGAAAGAGGAAATC[C/A]TTTTCTTACTAGAGATTTTTTTTCCCTTTAATCCTTTCAAAAT TCAAGGATCATCAAGGAGCAGGTGCAGAGCTCTGGGGCCAGAGGCCCAAGTGCTA
WI-18409a	20	C A ---	---	AAAAAGGAAAAAGGATGGAGTAAGAGAGAGAGACAGAGGAAACAAAAATAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAAAGGAAACACAGAGAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18442	62	C T ---	---	TTGATGTTAATACTGTCATTCTGGAGATCGGCTAAAAATG[A]AAAGCATAGTTATTATTAGCTTTGG TATATTCTGGACAGATTTAAACAAGTAAGACATATATCAACCCTCATATTTTCCAAACA
WI-18452	38	G A ---	---	ATATAAGCTGGAGACTGTGGAGGTGAGAGGAGTGGGACTAGCTGTTGAAAGAGAGATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAACA[A/C]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
WI-18489	102	A C ---	---	CTGGTGGGAGGAAACAAATTTGGTATATTTCATACAAATGGAAAACTCTTCAGAAATAAGAAAGGAA CAACCACCTGAATCACACAACATGGACAAATCTCAATCATTTATGCTGATGGAAAGAAACCATTCAC TAAGAATACACAGTACAT
EST5b	93	A ---	---	

EST5	93 A	---	---	---	CTGGTGGGAGGAAACAAATTGGTGATATTTCATACAAATGGAACACTCTTCAGAAATAGAAAGGAA CAAAACCACTGAATCACACAACATGGACAATCTCAAATCATTATGCTGATGGAAAGAAACCAATTC TAAGAAATACACAGTACAT
EST6	48 C	---	---	---	TTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAGCTTTTCTTTCTTTTGCACAAAGACAAAGCAAGCCACATTTTGCATTAGACAGAT
EST8	158 A	---	---	---	GGACAGGACCTTATTCOCGCTGTGCAGCAGCGGTGATGGACTGAGGCCCGGAGGATAGTGGGCG CTCTCTCAGGGGCTCTCCAGGACCCAGAGCTGTCTCTGTTGAGTTTCCCTAGAGCTGTGCGGCCA GATAGCTGTCTGAGTTGCAAGCAGATGGAGATTGGACACTGTGTCTTTGGTGGGT
WI- 18740c	104 GT	---	---	---	TCCTCAATTGTTGGGATGATGAGAAGAAATGATTTGGGAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAACTCATTTACCATCATGTATCCAGTAGTG[GT]ATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 CG	---	---	---	TCCTCAATTGTTGGGATGATGAGAAGAAATGATTTGGGAAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAACTCATTTACCATCATGTATC[GT]AGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 CT	---	---	---	CCAAAGTCTCTGTTGCTCATAAAGAGTTTGGGATGGGAGAGATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCCTTTCATTACAGAGGTAGCACAA[GT]GATTCCACACAAAACCCCTTCCCC TTTTAAATGATTCTGTTCTAATGCCATAGATCAAGGCCCTCAGAAACCATTTGTGTTTCCCTCT TGAAGCAATGACAAGCACCTTACTTCACGGTGGTTTGTCTTTCTTAT
WI-18746	114 GA	---	---	---	GCCAGCAGCTGAAGTCTCTTTCTCTCTCTGCTGGAAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGCTACTTGACCGTTTTTATATTACTTTTGTAAATATCTT[GT]ATCCACATTTCTACTTCAGCT TTGGATGTGGTTACCG
WI-19112i	212 GA	---	---	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCCTGGTTACGGCCCGGGGGAATATGCCAAGG GACCCCTTAATGGAAACACAGATCAGTAGTGCTATCTCATGACAACCAAGAAACCCGACGACAAA TCCTTTGCGAGATTTCTCTAGTGGCTTAGAAACATGGCTTTAAGAAACACACGGTGATATCTTTGAG GGTGACAAGGC[GT]ATCTCTTCAACAGTCCATACCAACTGCTTTGCTCTAG
WI-19092	232 AC	---	---	---	TGGTGGCTGGCTAGTAGTTTCTACAGAACATAATTTGCCTCTATAGAAGGCTATTTCTAGATCATGT CTCAATGGAAACACTCTCTTTCTTAGCCTTACTTGAATCTTGCTCTATATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGTCTTTGTATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTTC[AT]ATGATTAGCCGTGTAAC
WI-19057i	175 GA	---	---	---	CCCATTTATTAGGCCAGTGATGTCTCAAGAGTAGAGGAGCGTCTACTGGTCTTTCAACTCCTTCA GTCTTCTGACGGCGACTTTACGTGACAGCGGAAGTGTATTGTACGTCAGGCAACCGCAGCCACTG TCTTCATGCAAGGAACACAGTGCCAGATCCCCACAGCTC[GT]ATCTTCTCACTTGTGTTTGGCCACA

WI-20103	168 C T ---			TGGGACTTCCAACCTCAGAGGATGTGGGAATCCAGCTCAATGATACAGGATAAACATGGGATGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTGGGCTGGAAGCTGGTCTCTCCCA/C/TTTCAATCTGCTCAAAGCTTCTTGAAGGAGC TGGTTTGACTTCAACTTGCTAGAGCCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111 G A ---			GCCTTACCCATTTGCACATATATACATATGCACCACTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTTGAAGGACAAGAAATGGA/G/TTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTTCACTACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116 A G ---			TGGTTACAAACCTAAGCCCATATACAAAATTAGAACACATTTAGATGCCTCTTTTGAAAGAACGT TTTAGTCTTTTAACTGAGTTTAAAAAAAATAACAATGCAATTTTTTA/G/ACACTGTTTTTGA ACTTAAAGTGCAGCAATA
WI-20613c	165 A G ---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAAATGGCATGGAGGAGGAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAA/G/AAAGGGAGTTTCCACGACGCCAGTGGTGAGC TGC
WI-20613b	156 A C ---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAAATGGCATGGAGGAGGAGTTAGAAAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGAA/G/AAAGGGAGTTTCCACGACGCCAGTGGTGAGC TGC
WI-19984	47 A G ---			CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAATA/G/TTATAACATTAGAAAA GCAAAATTTCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTTCCACACTGGAAATGAAGGCAGTTTTCCAAATCTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135 T C ---			GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCAATCAGGCAATA ATTGTTTCTTGGAACTCTGCACCGACTGTCCATGCTCTGTGGGGACTTACACATTCAAGTTTGACAG T/C/JTGAANAACCAACTGGAGCTGCTTTTCCAAAGATGTTCTGTGTCCTTCAAAATAGGAATTCATG TTATTTCTTCTTGGCCTTAAGCTCTTATATCTTTCAAAATGACCTAAGCTGA
WI-18846a	49 G A ---			GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCCT/G/AAAGCTGGGAGCGT GGGCTCAGCAGGCTGTGCTCCATCCCGTAAGACCTCCTTCCCTTCCCTCAGCAGGCCAACATG GCCAGACTCCTT
WI-18959	123 G A ---			AGCAGTGGCCTTATGTCATCCAAACCCAGCCTCTTGACAGGCTGCCTCCTTGTGGCAGCAACGGC ACAGCTAATTTACTACAGTGTCTTTAAGTGAATAATGGTCGAGAAAGAGGCACCG/G/AGGAAGCCG TCCTGGCCTGGCAGTCCGTGGGACGGGATGGTTCTGGCTGTTTGAGATCTCAAAGGAGCGAGCAT GTCTGGACACACACAGACTATTTTAGATTTCTTTTGCCCTTTTGCAACC

WI-20146	31	T C ---				<p>TGAGTCTTCTGTAAATTCATTGAGCAGTTAGCT/C/CATTTTGAGATAAAGTCAAAATGCCAAACACTAG CTCTGTATTATATCCCATCACTACTGGTAAAGCCTCATTTGATGTGTGAATTCATACAGGC</p>
WI-18922	74	G A ---				<p>TAGGAATTGGTTTCACGCCCTGAGGCAATTAGACACTTTGGAAGATGGCATAACCTGTCTCACCTGGAC TTAAGC[G/A]TCTGGCTCTAATTCACAGTGTCTTTCTCCTCACTGTATCCAGGTTCCCTCCCAGAG GAGCCACCAGTCTCTC</p>
WI-18763b	53	A G ---				<p>TTTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTGA/G/GTATTTAGAATG TACCATAATTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGTTGATGAAACGTCA TGTGTTTTGCCAA</p>
WI-18763a	38	A G ---				<p>TTTCTGTGTGTGGGGTCAACCGTACAATGGTGTGGGA/G/GTGACGATGATGTGAATATTTAGAATG TACCATAATTTTGTAAATTAATTTATGTTTTCTAAACAAATTTATCGTATAGTTGATGAAACGTCA TGTGTTTTGCCAA</p>
WI-18771b	75	G A ---				<p>CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAGAGATGTTGGG AACAGAA[G/A]AAATAAACTGAGTTTAAGGGGACTTAAACTGCTGAATTCACCTGTGGA</p>
WI-18771a	57	A G ---				<p>CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGGATGCCTAG[G/G]AGATGTT GGGAACAGAGAAATAAACTGAGTTTAAGGGGACTTAAACTGCTGAATTCACCTGTGGA</p>
WI-18820	70	T C ---				<p>GGGAAAAATTTGAGACGCAATACCAATACTAGGATTTTGGTCTGGTGTGTTGATGAAATTTCTGAG GCCT/C/GTGAATTAATCTTTCATTGTATTGTGATTTTCTTTAGGTATATTGCGCTAAGTGAACCTT GTCA</p>
WI-18742b	51	C T ---				<p>ACAAAGTCTGTAGCCCCCTCACCTTTCTGTTTTCACITTTTGCCAATGTAC/C/TJATCGGGTTTGGTTT TCTTGATTAATTTAAACGGTTGTGGTTTCTTTTCCACGGAGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC</p>
WI-18882	94	C T ---				<p>GTGTGTCCAAAAATGGGGTCTGCTCTGCTACCTTGACCCCTCCCTTCCCTCTGCTCTCTCCTCATCA TCATTTCCCAACAACATCCTCTGCCA[C/T]ACACAACAAAAACGTAAGTTTCATTTGGGCCAAAAATTGA GC</p>
WI-19970b	167	G A ---				<p>TATAAGCCCGAGTACCAGGACGGCCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCACC GGCCCCGGCAGTCCAGCGGGGAGGAGGCTGCCGTTCTCTGCCAGTTCCCTCACTGCGGGGAGC AGCAAAGGCCTTCTCACTGGTGGTCAAAAG[G/A]TAGTCACCTTGGCCCTGGTGATCCACAGAGGA TGTGTTCAAACCAGAAATCTTTTAAACGACTGACCTTCTTAAAAACAGA</p>
WI-19970a	126	T C ---				<p>TATAAGCCCGAGTACCAGGACGGCCTGTCTGGCCACAGACAGGGGCTGCCTGTGGAGCCTGCCACC GGCCCCGGCAGTCCAGCGGGGAGGAGGCTGCCGTTCTCTGCCAGTTCCCTCACTGCGGGGAGC ACCAGCAAGGCCTTCTCACTGGTGGTCAAAAGGTAGTCACCTTGGCCTGGTGATCCACAGAGGAT GTTGTTCAACACCAGAAATCTTTTAAACGACTGACCTTCTTAAAAACAGA</p>

WI-19067d	202 T G ---	---	TATTGCTGTGCTGCTGACATTCACGGCAAGGCTGCTGACGCTCCCTGGCTGTGC ACATTCCTCTGCTCCACAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTTCTC TTGGGCTCTAGGCTCGAGAATGTTGTAGGGGTTATTTTTTAAATAGTGTTCATAAAGAAAT/ GACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGTGCTGCTGACATTCACGGCAAGGCTGCTGACGCTCCCTGGCTGTGC ACATTCCTCTGCTCCACAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTTCTC TTGGGCTCTAGGCTCG/GC/JAGAATGTTGTAGGGGTTATTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGTGCTGCTGACATTCACGGCAAGGCTGCTGACGCTCCCTGGCTGTGC ACATTCCTCTGCTCCACAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTTCTC TTGGGCTCTAGGCTCG/JGGAGAATGTTGTAGGGGTTATTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGTGCTGCTGACATTCACGGCAAGGCTGCTGACGCTCCCTGGCTGTGC TGCACATTCCTCTGCTCCACAGAGACTGCTCCGCCATCCACAGATGATGATCTTCAGTGGTT CTCTGGGCTCTAGGCTCGAGAATGTTGTAGGGGTTATTTTTTAAATAGTGTTCATAAAGAA ATACATAGTATTCCTCTCAAGACGTGGGGGAAATATCTCATTATC
WI-19106	247 T C ---	---	TAAATCCAGCCCTACCTTGTAGTATTTTAGGAGACAGTCTCAAGCACTAAAGTGGCTAATTC AATTTATGGGTATAGTGGCCAAATAGCACATCTCCACGTTTAAAGACAGTGGATCATGAAAAGT GCTGTTTGTCTTTGAGAAAGAAATAATTTGTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGGCCATAGCCTATAATTGGTTAGAACCTCTCTATTTAA/JCTJGG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTACACACCTACTAAAAAGTTATTATGTAGCTGAAACAAA AATGCCAGAGGATAATATTGATTCCTCAGATCTTAACTTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAAC/JG/JGTTTAAATTAATTCACAATATAAAGTCTACAGTTAATATGTGCATA TTAAACAATGGCTGGTCAATTCCTCTCTTCCCTTAATAAATTAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATGGATGATTGTTCAATACATAAA GTTCTCTGTAATTACAATAAATATTATGCCCTCTTCTCAGAGTCAAAAGGAACCTGGGTGGTTGGT TTTTGTGCTTTTTTAGATTTATTGTCCCATGTGGGATGAGTTTTAAATGCCACAAGACATAATTTA AAATAATAAACCTTGGGAAAGGTGTAA/G/JACAGTAGCCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGCTAGCCTCAGAAACTGGAATAGCCTTCGAAAAGAAATGTCTTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTTGTGCTGATTTGACCTTGATTTCAAGTTAACTGTTCCC CTTGGTATTTGTTTAAACCTGTACATACTTTGAGTTCA/JCTJTAGTACGTGTGGCTTGGTCA CTTCGTGGCTGAGGTAGAACGTGCTTGTGGAAGACAACTGTGTGGCTTG

WI-19042	193 A C ---	---	---	TTTGTGAGTGTGCTCGGAATGCCTCAGTAGCATCTCAGTGGTGTGAAGTTTGGAGATAGATG GATAAGGGAATAATAGGCCACAGAGGTTGAACCTTTGTGCTTCAAGGACATTGGTGAGAGTCCAACAG ACACAAATTTACTGCGACAGAACTTCAGCAATTTGTAATATGTAATAACTCTAACCACAA/CJGGCTG TGTTAGATTGATTAACATATCTCTTTGGACTTCTGAAGAGACCACCTCAAT
WI-18984	208 A C ---	---	---	ATTGGCCCTGTACAGTTTGCTTATTTATAAATTCATTAACACACTACAGGTGTTGAATGGTTAAAA TGAGGCCCTCCAGTTTCATTTTCAGTTATTTTCGAGTGTGCAGACAGCTATTTCCGACTGTATTAAT GTAACCTATTATGAATCAAGAGCAGTAGACAGATGTTGGTGAATACAAATATTGTGATGCATT TATCTT/CJATAAAATGCTAAATGTCAATTTTATCACTGCGCATGTTTGACT
WI-18851	90 T A ---	---	---	GCTTCAATTTGGCGATTGATTCAGTGCACCAATGTAACAGGGTTGGTAGTTGTACTCATTTTGAAT ATACCTTTTCCCTATTGATTTCT/AJGTAATATAGGATCCTGGAAATGAGACCTGGTGGA
WI-18821b	76 T C ---	---	---	TCAACTGCAAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT/CJGGGGTAGCCATTGTGCAGTCATGGCCCGGGGAAACTTGCCAACCTTCGTGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---	---	---	TCAACTGCAAGTGTGCTTCCCTCCCTATAGGGCTGGAATCTGTCTAGGAGCCCTCTCTCGGAGGCC A/CJTAGAGGCTGGGGTAGCCATTGTGCAGTCATGGCCCGGGGAAACTTGCCAACCTTCGTGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---	---	---	ACTCCTCTGCTGTCCATC/GJACTGTCTCTTTGAACCAAGGAAAAGTCAACAGAGTTTAAAGAGAA GCAAAATTAACATCCTGAATCGGGAACAAAGGGTTTATCTAATAAAGTGTCTTCCATCACGTTG CTACCTTACCACACTTCCCTCTGATTTGCGTAGGACGTGGCATCTACTTACGTACGTGGCATAAC ACATCGTGTGAGCCCATGTGCTGGGTAGAGCAAGTAGCCCTCCCTGTGTC
WI-18908	70 G C ---	---	---	TGGAATTCCTTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG/CJTTAGGGAACATTCATCCTTGAGTCAAAAATCTCAATTTCTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---	---	---	CACGGTCTCTGCATCGTTACCAGAGCGCCTTCTGTCTCTAGCCAGCCCTGTATGACCGGCAATA TCCCCAAAGCTTTTGGGTCTCAAGTCATGCCCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA/AJGJAAACCCAGCCACATGACTAGCAGCTGAGCTGTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGAGGTGG
WI-19037a	47 C A ---	---	---	CACGGTCTCTGCATCGTTACCAGAGCGCCTTCTGTCTCTAGCCAGCG/CJCCGTGTATGACCGGCAAA ATATCCCCAAAGCTTTTGGGTCTCAAGTCATGCCCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCTCCCTTACGAACAAAACCCAGCCACATGACTAGCAGCTGAGCTGTGCAGGGACCA GTGCCAGGCACTGGGGGTGGAAGTGTGGTGACACAGTGAATGGAGGTGG
WI-19064	66 T C ---	---	---	TTGAGGAGGTGGGTGAAGTGTCTCTTGGCAGGATTTGTGACACTGCATTGCTGGGCTGTGTTCCT/ CJCGGCTCTTCTGGACCTTGACCGTGGATACCGGCCATGTGCCATGGTATTGGGTCTCTGGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---			AGGCTGTGGCTTATGTCAOCCACAGAGGGTCTGAGAAGTCTGGCTGGGATGCCCTGGCC CCCTCTGGAAGGCTCTGCAGATGACTGGGCTGGGAAGCAG[AG]TCTTGTCTGGCCATGGAGCC TCATTGCAAGTTGTTCTGAACACCTGAGGCTTCTGTGGCCACCAGGCACTACGGCTTCTCTCTOC AGATGTGCTTTGCCTGAGCACACAGACAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184 C A ---			GTTTGCAAAACCAACATGTGCTCTTTTTCAGTCATTCACTGTTTAAATGACATGGTAGAGAATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTTTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCACTCAAC[CA]CTCAACACTATTGAC TTTTGGGCTGGATAGTTCTCTGTTGTGGGGTTTGTCTTGTGCACTGTAG
WI-19016a	161 C T ---			GTTTGCAAAACCAACATGTGCTCTTTTTCAGTCATTCACTGTTTAAATGACATGGTAGAGAATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTTTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAACCTTAGATACATAGCCG[CA]TGTATACAGAGGTTCACTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTTCTCTGTTGTGGGGTTTGTCTTGTGCACTGTAG
WI-20096	21 T C ---			GGTTTGGGGCATTATTTCT[CA]GATAGAGACTGGCACAAGCTTTGGGCTAAGGACACCCGCCCCC ACCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---			TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGTAACTCCAGCCATG AGTATAAGATTAAAGCAGTTACTTTTATTTGAACAGGAAGTGGCATAAGCAACTCAGTGTGCC CTTAGGGTGGGAGCTCTTCC[CA]CTACCACTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---			TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGTAACTCCAGC CATGAGTATAAGATTAAAGCAGTTACTTTTGAACAGGAAGTGGCATAAGCAACTCAGTGTGT GCCCTTAGGGTGGGAGCTCTTCCCTACCCTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---			TCCTCCAGCTCTGTATCCTTGTCTGAGGGTTCTGTGTTACGGCCCTCCAGGCATGGTTTCTTCAT TTAGGTAGGAACAAAAGGCCAAAAGAACATACAAAGCCAGCTCTCTAGAGGCTCCA[CA]TCAGAA CTGGACCTTTAACTACAAAGGAATCTTGATGAATTTTATAGCGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGACACTCAGGCCATCTTCTCCCAATGTCTCCCGGGGG
WI-20860	224 G A ---			CTCTCCCTAAGGAGCCTTGGCTTGACGCCCTTCAGCAGGATGGAAGTCACAGACAATGAGT GGAGCCTCATGCCCTCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTATCCTGCTCTCTCT CCCAAGTGTCTACACTTGGCAAAAGCAGAGTGGTGGCAGACCCAGCCTTGAGAGCTCTTGAGACC GGAAGGAAGGGCGGTCAIT[CA]AGGTGATGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---			GACGTGGACAAAGGAGGTTTAAATGAATACCTTGTGTTTGT[CA]GATGTTCAAAAAAGAGATTAAAT ATTTGTGACTGCATCTGTGAATGAAGACACTCAAAAAGCCATGTTTCCAACTTAGGTTAATAATAA GGCTATTGTCCACCACTCTTCGGGCAATGCTGCAATATCTGGGCTCAAGTGGGAGGCCACGTG GGAACAGGCCTCAGAAAAACAAGGACATGCAGCCTCCCTGAGCCAGTTCT

WI-19766b	93 A G ---	---	TGGCCTCAATGACTGGTACATTGGAGAAGCTGTGCAGCAGCATCCTTTTCTGTGGTGGCAGGGCAGG AGATGAACCATAGGAGCCAAAAGTC[A/G]GACAAACAGAAGGACACACCAAGCCTGAAACCCCTC CGGACAACAGCAGAGTTACAGCTGAGGGATGCCCTGGAGTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTACCCCTCCTCTACACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---	---	TGGCCTCAATGACTGGTACATTGGAGAAGCT[G/A]TGACAGCAGCATCCTTTTCTGTGGTGGCAGGGC AGGAGATGAACCATAGGAGCCAAAAGTCAGACAACAGAGAAGGACACCAAGCCTGAAACCCCTC CGGACAACAGCAGAGTTACAGCTGAGGGATGTCCTGGAGTTTCTGACCCATGAGAGGCCCCCTC ACCTCCTTACCCCTCCTCTACACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---	---	CTTCTCTGTTTGGCTTTGCAATTTGTGCGATTGGAAAACCACTTGGAGAAGGGACTTTTCTTGCAA AACCTTAAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGACTGA[C/G]AAAGC TTAGAAAGGAACCTGAAATTGCTTCTTTGAATATGGATTTAGGGCGGGCGTGGGTGAGCTACGCCCT TATTAATCCAGGCACGTTGGGAGGGCCAAACGGGGTGGGATCACCTGA
WI-20512c	59 T G ---	---	CTTCTCTGTTTGGCTTTGCAATTTGTGCGATTGGAAAACCACTTGGAGAAGGGACTTTTGTCTCTG CAAAACCTTAAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGC TTAGAAAGGAACCTGAAATTGCTTCTTTGAATATGGATTTAGGGCGGGCGTGGGTGAGCTACGCCCT TATTAATCCAGGCACGTTGGGAGGGCCAAACGGGGTGGGATCACCTGA
WI-19599	230 C G ---	---	GGGCTTAAATTCCTCTGTTGGGACTGGTCTCTCCAGTTTACAGCAAGGATCGCACCTTTTCC ATAACCCCTTCTACATTGGAAGAGACACACCTTGATACAGAAATGGCTCCGTGAAGTCTTTTAAACG GACAAAGGTAATCACAGCTAACAAACGATGATTTGGCTCACACGTAACCAACACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGGCA[C/G]TTCCAAGAGTAACACTGCTA
WI-20679	82 T C ---	---	TGTTTGAATAAAAAATTTCCATGGTCTTAATTGAACCTGATGTTACTTTCTTTAGAATAICCTTTT TTCATTAAAAATAAT[C/G]TCTAAACCACTCTATGTGTTCAACCTTCTGTTTACACTAAGATATGGGT TTTTGGAAGGCCACAAAGTCACCAAGCTCCATGAAGTGGCGAATTGGTCTTGTTTGGAAAGCTCTC CAGGGTGTTTCTCCAGAA
WI-19909a	29 T C ---	---	CCAGAAATAAAGCCTGAATATCTCTTTT[C/G]TTAAAAATAAATTTTCTCTTTGCTCTTCCAA GTAAATCTTAAATGAACCTGTTCTAGTCTATTTTAACTAGGCAATTATAACACTACCTAGGCGGG TTTTTCTTTTATACCTTGTTCTGACTGTGGAACTCACTAA
WI-20341	221 G C ---	---	TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAAGTCTTAGGGCATGAGACATTAGGAAG GCCACAATTATGAGTAATGAAATGTGGAGGCTGATGAGAAGCTACTGCTCCCATTTGTTAGCAGGA GGCAGGAAAAGTGATCTGGGGTCTCTGGCAGCAAAAGCGTGTGTAATTTGGGTGACGTCATGC ATCCCCCATGCATTGGTTT[G/C]ATGTCCTCCAGTGAGCTGTTGGGCAAGTCT

WI-20113	60	T C	---			TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATACTGT/CIGGA AACAGTAAAGCAAAATACACACAATAGGAGGAATTTTTCAGACATAGGATAATTTAAACAT CACTCAATACTGGAGCATGATCAGCAATAAATCTATTCCATAAACCAAGTAGATAAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTATT
WI-20895	107	G C	---			TGATGGCAAGTACAAAGGCTCTGAAAGAACAGAGTAACAAGAGCAGCGCAGTGCGGTGTGGC CACTTCCACACAGGAGAACACTTGACTTCATTAAAGGAAA[G/C]CTTTACTCTGTACTTTTTCCTC CCACATAGTTTAAACCCAAATAGAAAGGCATTCTATTCTCAGACTACTGCTCTCTAAGGTCCTAGGAA TATAACTGGTACTATAGGCAACAGATGCA
WI-20721	72	T C	---			CCTGCAATCACAAAAGTGGAACTAGTTGATATTTTGAATCATACTTGAATTAACCACTTCAGAAA TTCTAT/CJAAAACACTAGCAACTTCTTTTATCAGA
WI-19415c	161	A G	---			CTGGATTTAATAATTTCTGGCCTAATAACCAATGTAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTGAAGATCCCTAAGTAAGGTATTGACGACTGAGACTAGTCCGGCAAA GTCATGAGACCCCTTAGCTGATCTCAT/GJAAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCTCG
WI-19348c	103	C T	---			GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTAGGCGCCATGCACCTTCTG GCGGTGATGAAGAGACTGTTGGTCATGGCGTG/CJTGCTTCTCCAGGCTCATATGGATGTCT CGAGTTGCACAGGGAAGTCTGCTCTGTTGTAGAAGCTTCTCC
WI-19348b	98	G A	---			GCTGCTACTGGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTAGGCGCCATGCACCTTCTG GCGGTGATGAAGAGACTGTTGGTCATGGC/GJA/GTGACGTCTTCTCCAGGCTCATATGGATGTCT CGAGTTGCACAGGGAAGTCTGCTCTGTTGTAGAAGCTTCTCC
WI-19635	98	A T	---			ATTAGTTCTGTTGGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAACACAATG TTAAAGGTACAGTAAAAATACAGTATTAT/ATCTTATTGTAGCACGGCTGTGAGGCTCAT GTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGTGCTGAAAAGAACTTTGCCTT T
WI-19641a	46	A G	---			TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAG/GJATTATATAGTCTCATGTTT TTAATTTATGAATAACGCTGATTCATTGATTTTGTATTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAATAATGGATCAGAGTAGTAAGTCAAGAAATAGTGCATAATGTGGTTTAAATTTAAAA AATACTCAGAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52	C A	---			ATATAGAGTACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCCCT/CJ/JGGGTAACCCAG GACTATTGCATGAGCATTCITTAATACGTATTTTGTAGGACACAAGTTTTCATGCTATTA
WI-19673b	180	C T	---			TCTGCCATGATCACATTGTGATGAAGAACATGATGGTCACTAGTAGTAACCTTCTGTGTCATTGCCT TACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGTCATCACCACTGTAAATCTAATAGT GAAAAGGCAATGATGCTCAGTATCACTGTGAAAACATTTTTC/CJ/CTTGGACCACTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACAGCTCAAAAAAACACAGCCC

WI-19673a	35	G A ---				TCTGCCATGATCACATTGTGATGAAGAACAATGATG[A]JTCAGTAGTAGGTAACATTTCTGTGTCATTG CCTTACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTGCATCACCACCTGTAATCTAAT AGTGAAAGGCAAAATGATGCTCAGTATCACTGTGAAACATTTTCCCTTGGACGAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCAGTCAAAAAACACAGCCC
WI-19724	35	A G ---				TTTATTGGAAACAAAGGATTGTAATTTGGTAA[A]GJCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTTGGTTTTCTCTT
WI-19307	196	T C ---				TCCTCCTCCCCAACTAGATGATTGATCACTCTGCCACAATGGTACCCCTTCAGCAAGAACTG CAAGCCCTTCTTGATTGCCCTTCATGAGAAAATGGTGGCTGGAGTGGAGTGACATTCCTTGCTGT GGTGAAC TGCAAGAAAGGAAACCAAGGCAATGTATTCATAGAGCCCTTTAAAGAGACCCG[T/C]TGG AAATGGGCCATGGTCTAATTTGGTGTGAAATAAACTAACCTCTTTGGCTG
WI-19269	85	A T ---				CTTCCCTCATCCCTCTTCCACACACCATCCCGGAACAAGTGCTCCAGGATTCCTGCCACTGGC CATTTTGGAGTGTGCC[A]/TJTTGGGTAGCAATGTGGAACCAACAGGGCTTTGTGGAGAAATGG AGGGGTTGAGGGAGTCCAGGAGGGCTTATTTGAGGGCTTTGCCACTTGCTCATAGGGGAGCTCG ATCTCCTCATCATCTGGACAGGTGGAAGCAATCTTCCGGGGCTAGGCA
WI-19946	122	C T ---				CAATGGACTGAATGAGTGCCTGGTGGGTGGGGCACACACACCTTCAATACACGTCGAAGGTGG CTTCCAGTTTGTAGAAACAGAAATCTGCATCTCAGCCTGAGACGCACAGAGAGGT[C/T]TCTTCCCTG ACCCAGACGCACTCACGAGCCAGTCTGGTTTCAAAAAGTCATTTAACCTGCGCCAGAGAGTTTCA CGTAGGCATCTTTAATAAATACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	G A ---				CACAGCATGGTGTAAATAGCATCAGATTGAATGAAAAGTTTGTAAATGCAACCATAAATAATATA ATAAATATACATCAAGTAACTTTACAGCACACATTTTGTAGGCCAAGTTTGGATCTGTCTGGACCT CAATGT[G/A]JCTCTCGGAGAGCAGCCAGCTTAGCAGCAGATACCTTACAGCTTGTCATCTACTCAA GTGATGGCCCAACAGAGCTTCTGAACCTCTCTGGGGAGGTAGCTGACAAG
WI-19076	40	G A ---				TTGGTTGGATACCTGCTGGAAAAAAGCAGTTTTAAT[G/A]GTATTCAAAATACCTTTTAAAAA GTATTTAGCACAAAGATTTTCTGTAACTAGATTATGTGTAAACTTTTTCTAAATCTTGTAGGAG TGTCGGTTGTAAAGAACTAGAGCTTATCCTATTCCAAATCTATCTGCGCTCTGAAAAAAGTGCAGA AAGGCATTTGAAAGCTGTTCTTTAAGATATGGGATTTCTTTTATTCTT
WI-20218	26	T C ---				CCACACACTCTGGTTTTATAAGCTA[T/C]JAGGACAGAGCAGATGGAACCTGAAAAACAGGGTAG AAAAACATAAATTTGGAGGGGAACAGTGGGATGCAAGAAAGAAATGACAAACAGCCACATGTGCCCCA GTCAAATCTTTTAGTCCCTGCAGCAGAGATGCCAACCAAGTCTCTATACTGGCTGGGATCTGCCC ATGGATGCAGGAGAAAAA
WI-20295g	154	T G ---				CAACCTTTTGACAAGGGGACGTGAATTTCTGATGAAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAAATATCTCCAGGCTTGAATGGGAGGGGCTGGCTCTACCCCTTCTTCTTTCCA TCCAGTCTATTGCCAGAT[G/C]CAGAGAAAGCGGGAGGCCAGCTCTCCAGCATAGCCACTGTGG GTGCGCTTCACTCTCTGTGGACTCTCTCATGCTGGACTTGCTTTCTGCTTCTGCGG

WI-20361a	192	G A ---	---	CTGGAGTGTGACCTAAGTGACATTTTTTTTAAATGCCAAATACAGTAATCTCCAAGCTTTTAAATGG CTTATGCAAGATGACAGAATATGTGAAATCTGATTGTCCAGAGTTACACTCTGCAGCTCCAAAGCTA CAACAGTCCACAGCTGAGAGGTTCCCTATACCTTCTACTACTGTGACAAATTAGC/GAATCCTTC AAATGGGAAATTCCTAACTACACGAGACAATGGGTCTCTACAGTAGGCCGG
WI-20572	75	A G ---	---	GAGCCAAACCCAAAATAAAACAGAACTCTTTTGTAACTAAGTCATACCTACTTTCTTCT TCAGAAATTA/GTTCATAAAACATCATCTTTACAACATGGAGAAGCGAGGTAGGCCATAATTTGTTCA AATTCATCTTTCTCAAAATTTAAATTTGTTTTAATCCCAAAGGTGCCTATTGAATTTCTTCAAAAATA AACTGCCTATCAGGTATCATACCTGCAAAATGCTTCTAATATCTCTTGATTAT
WI-20588	133	G A ---	---	CATGACAAAAGACAAAAGATCAAGGAGTAACATAAATTATAAGTTGAATAAATAGTATACAGCAATC TTCACTTTTTAAGAAAATGTGAGATCCTTTGTTGGTTTTTATTCCTTAAGTACAAAATGCTAAACI G/AJGGAGCCGAGCTCTCCGCATTACAGG
WI-20593	79	A G ---	---	TGACCTCATACTGGTCTGGTTAGAACACAGCCACTAGAACAACTCCAGCTTTTTCAGTCTGTTG CTGTACTTCAG/AJGTTTAAATCTGGGAATGAGCATGCGAATGCTCCAGATGAGGAAGAAA AGCTGTTAAAGGAACTCAGGATGTTGTTAGGAAGGGGAGTGATGCCAGGCCTTCACCAGACTAT CCAGAAGCCATTCCATGGGTATTTGGTCTGCATACCTGTGAGACACTGAGCT
WI-19765	57	T C ---	---	TTCTTTGCCAAGCCTGTTCTTCAAGTTATTCAGAACTGGGTGTATACCTTGCTCTCAJTC/JATGTATCT TGTCCTGCTGCTTTTAGTTAGCAAGGTGTATGAATACTTTTAAAGTTTTGTTGTTCTTTTCCTCGT GGTATCAGTGAATACTGATCTATTCTCTGGCTAGGTCAATTTACAAAATTGCCCATGGAACTGAGC AAAAGCCCCACGTGGGATAAAATCACTCACCATCGAGCCCAACAGTATT
WI-19066i	239	A G ---	---	TGACAAGGGAGAGAAGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGGAACTGG CATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTTCCATATTCGGGATGCTCAATTACAGT ACCATTCAGGGCAAACTTTTCTTAAACGCCCTTCACTA/GJGTTTCTTTTAA
WI-19066g	184	C T ---	---	TGACAAGGGAGAGAAGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGGAACTGG CATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-19066f	148	T C ---	---	TGACAAGGGAGAGAAGGGAAATTCCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGGAACTGG CATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATTAATCTTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA

WI-19066e	147 G C ---	---	TGACAGGGAGAGAGGGAAATTTACTACTTTCATTCGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCATTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCATGCAATCTCTACGAGGAATGG CATATGTTCTTGCG/CJTGGTCACCCCTGTAGCTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-19066c	100 G A ---	---	TGACAGGGAGAGAGGGAAATTTACTACTTTCATTCGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCATTAAACCCCATGAACCTTCAGCTGATCG/CJTCTTAGCCAGTCCAAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-19066b	87 C T ---	---	TGACAGGGAGAGAGGGAAATTTACTACTTTCATTCGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCATTAAACCCCATGAAC/CJTCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-19066a	72 C T ---	---	TGACAGGGAGAGAGGGAAATTTACTACTTTCATTCGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA/CJTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAAATCTCTACGAGGAAC TGGCATATGTTCTTGCGTTGGTCACCCCTGTAGCTGAATCTCTCCATATCCGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTAA
WI-20660	105 G C ---	---	TTTACAGCGAGTTTTCGCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAAGAAATGTG TGCTAAATAAAATCTCCCTTTTGAATGTATATTTG/CJTAAATAAGGGAAGCATTAAATATTA CAGACATATTTACAAGGTTCTGAACATGAGTGATCCATTCTGTCTGTACAAGATAGAACAAA AAGCTATCCACCCGCCGCCAAAAAATACTGTTTAAACACACTATGTTTAAAGA CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGGCGGTCTCTGGCAGCCTCCCTCAGTCTTCC TCCACCCGCCCTTCTCTCCAGCCTGCCTGCATGATGTCACCCCTTGTC/CJTTCGCTCCATCGCC TTGAAAGCTCTGAA
WI-18768	120 C T ---	---	TTCCCCAGGGTTCTGTATTGCAGTAAGCTCAATGTAGTATTTAACTTCTAGTTGCTTGTCTTG GTCCTTCTTCCAATGATGCTTACTAGAGAAAGCAATCAGACACAAATTAGAGAAAGCCTTTTCCATAAA GTGTAATTTAATGGCTGCAAAACCGGCAACCTGTAACTGCCCTTTTAAATGGCATGACAAGGTGTGC AGTGGCCCCATCCAGCATGTGTGTCTCTATCTTGCATCTACCTGCTCC
WI-19087	37 A G ---	---	GAAAGCCAGAGATTAGCCCCGCTTCGGCATCTGCAACCCAGGACAGAA/TTGCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACCTTGGAGATCAGAAAAATTCATATTTAAGCAAAAGTGATACAAACA CAGTGATTGGGAATGCCT
WI-18790	49 A T ---	---	AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCCTC/GJGTGGCCAGCCAGACACTCACCCACCTT CCCCAGTGGCCCCGTGGATCTGGTCTTAGGCTGGACAGGATTCAGAAAGACACCAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTCAAGCCCCCTACACTCAAGGCTGAGAGGGCCTCAGGAA AGTCA
WI-18987	35 G A ---	---	

WI-18919	26 C T ---				TGGATGAAACACAGGGATTCCGGAIC/TGCCAGACCCCAATTTATACCTTCTCTACAGTG TTGTTTGTGTTGTTGTTTATTTTATACITTTGGCCATACCAGAGCTAGATTGCCAGGTCT GGGCTGAATAAA
WI-18741c	64 G A ---				CTTTCTGGTCAAGGCTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTAATATGAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38 G C ---				CTTTCTGGTCAAGGCTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTAGACCTCG CTGGAGTTCAAGCTTGAATTAATATGAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23 T G ---				CTTTCTGGTCAAGGCTTGGACAT/TGCTCTCAGTCATCAGACAGAGTATCTCTGCTAGACCTCG CTGGAGTTCAAGCTTGAATTAATATGAAGTTAATTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170 G A ---				TCAGAAAGCAGACATGGCATCTGTTCCCTTGGTGTGTTGTTGTGTACCTTTACGAGACCTGAAT TTAGAATGCCAGTGTGCCAGAGTGAAGTGAATCTCTTTCAAGTAAAGATAGGCTATCTC AACACTGCTGAGTGATTCAATAACATATCAACCA[G/A]TAGCATTAAACCAATTTATTTCCCTGTCCT AGTGTCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCGAGCATGCT
WI-19212	46 T A ---				CCAAAGTTGCATCCATGTTTGAATTTCTGATGAGACTAGAGTGACAGT[A]GTTTCAGAACCCAAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATATGCAGATGGCCTATGGAATGACAGTGC ATAATTAAACACATTATCAAGTCTCTTACAAATTTATTTCCGACAGCATGTCAGTAAAGTAGACCCA ATGGGAGAGAAATGCCTGCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210 G C ---				CTGTTGAAGGCTTCTCAGGCAAACTCCAGCTTAAAGCCTAGACAGGTAAGACACACATTTGGATG GCAGCATGGTTCTTCCCATTTATGGCATGAAATATGTGGTTAGAATAAGGAACAGCATTAAT CCTTGCCAAACAGCCTCACTAAGAGGCTTTTGTCTGAGTCAAGCAACACATTTGCCTGCTCTGCC CTTGGAG[G/C]TGCAATTTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214 T C ---				TTGAAATCCAGTCTCCTGGCCCCCAGGCGGTCTGTACCATAGAAATGTCTTCTCTACTGGGTC GTTCTGGCTTTTGTAGAACTTGGTCTGAGATGTTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAAGACAATGTTTCTGTAATCTGAAACTGGAACCTGAACCAAGTTTGGCTTCTCTCTAGTCAAC AAGCATACTT[C]TCTCTGGCTCCCCAAGTACTTAATGTTCTCATCTGT
WI-19041	198 T C ---				GTCTCCCCAGAGTCTCTGCACCCCCAGCCCTGTCTGCTGTAAAGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCCAGGGGGTGCCTTAGTTGGACATGCTGGGTAGCAGGACTCCAGGGCGTG CACGGTGAGCAGATGAGGCCCAAGCTCATCACACAGGGGCCATCCTTCTCAATACAGCC[T/C]G CCCTTGACGTCCTATTTCAAAATAAAATAGTGTGTCTTGGCTGCTGTGT
WI-19135	20 G A ---				CAGTTACCTGCTTTGCCTC[G/A]AAAGTGTATCAATTTGTAATTTAGTATTAACCTCTGTAAAGT GTCTGTAGGTACGTTTTATATTAAGGACAGACCAAAATCAACCTATCAAAAGCTTCAAAAAGT TTGGGAAAGGGTGGGATTAAGTACAGCACAATTTGGCTTACAGTAAATGAAGTATTTTATTAAC GCTTTTGCCCATATAAAATGCTGATATTTACTGGAAACCTAGCCAGCTTCAC

WI-19236	54 G A ---	---	TACACAGAGGGTGCACCTTGGACTCTGAGGGTGGGTGTGGAAGGGGGAAGG[G/A]GATGGAGAC CTGCTCCCCAGCTCTTCTGTGAGCCGGTTTACATGGGAACAGGGTTAACATCTGTGTTAGGGAGGT CACCTTACCCCTTTTCATAGGGAAGAGTGCACACTCTGGCTATCTCAGGGGAATGGGAAAG AATCTTCAAGGGCAAGAACTCGTGGAGGATGCTGTGTATGTAATACT
WI-19144	222 G C ---	---	GTGCCAGTCTCCAGAAAGCAAGACTGCCCTTCATTACGCCCTGCTGACCTCCAGCCCTTCTAAGG CTCAGCCOCACGGGACTCTGTGGCTGCCAGCTTGTGAGTATCTATCTATATTCATTATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACACAGGAGGCTGTAGCCAGGAACCCCTCTCTCCCTGGT CTGGCTCTGCTGGAGCGG[G/C]TGGGAACCAACACCTTCAGTGTGGTG
WI-19139b	110 C A ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGAC GGCAGATGCCTGACAGAGTGGGTGGCAGACAACACTAG[C/A]ATTTACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGCAGCATGTGGCGTCTCTGTGTGAAGCCCGTCTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66 C T ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACACGAGGGTAGA[C/T]GGCAGATGCCTGACAGAGTGGGTGGCAGACAACACTAGCATTTCACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGCAGCATGTGGCGTCTCTGTGTGAAGCCCGTCTCTCTTTGG GGGGCCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112 T C ---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAAGGAAAGGGTGCCT CATCCCAAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGTG[C/G]GGCTCATGGCAGAGCATT CAGTGCCACGGTTTAGG
WI-19235	173 A G ---	---	TCAGGAGGTGGAGTTGCTGCTCAGCTCTCCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCTCTTCACTGCCCCAGTATTGCTCTGTATTTATCAGCGATGCCCCCTGT CACTCATGCCCTTGCCTAATTGTTCAACAATGGTGGAA[G/G]GCTTTCATGTAATATGATCAGGACCCACC TCCAGTTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTGCAGCACTA
WI-19222	179 C T ---	---	CGTTTTCCCTAACTCACCAGTTTAGTTGGGATGATTTGATTTCTGTTGATCCCATTTCTAA CTTGGAATTGTGAGCCTCTATGTTTCTGTAGGTGAGTGTGGGTTTTTCCCCCACCAGGAAGT GGCAGATCCCTCCTTCCCTAAAGGACTCTGCGGAAC[C/T]TTCACACCTCTTCTCAGGGAC GGGGCAGGTGTGTGTGTGACACTGACGTGTCCAGAAAGCAGCACTT
WI-19117	134 A G ---	---	AAATAATGCAACGCGAGGAGGAGAAAGAAATGCACCTAGACAAGAACATCTCTCATAGAACATTG ATCTGTTTACAGGAAACAACCTTGCTTGAATTTACACAGTGAGACTGTACATAATTGCATGAA A[G/G]TAGCTATTTTTTCTTAAGACATTTTTCATTCATGAATATTTTCAAGTTTTTCATACTGTACA CATTTCTTAAACACATGATACCAGCAGCAACTGAAATGAATGCCGAATTTG

WI-19134c	263	C T ---			CTCCTGTTCTGACCTGACAGGGTGACACAGCCCTTTACACTCTGTCTCTCTATCTTCCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCATCCCAAGAGGGGTGACGCCAGGGGTGAC GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGACGAGCTGCACTATCCTTTTCAGAGCAC TTCATCCACTTGCTCTCTCTACCTCGGCACCTGGGTGGGAAAGGG
WI-19134a	162	T C ---			CTCCTGTTCTGACCTGACAGGGTGACACAGCCCTTTACACTCTGTCTCTCTATCTTCCTGGGTAGA TGCCCTGGTGTAGGGCTGAGTACTGAATGGTCTTCATCCCAAGAGGGGTGACGCCAGGGGTGAC GCCCTTCAGAGCCAGGGCTAGAGGATGCACGGTGGCTAGACGAGCTGCACTATCCTTTTCAGAG CACTTCATCCACTTGCTCTCTCTACCTCGGCACCTGGGTGGGAA
WI-19224	112	C T ---			GGTTTCACCACTGTTCCAGGGAACCTCCGATGAAGTGTCCAAACAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAAACAGAGGAGATAATCTCTCAGGATGCCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTTTATAATCCAGCAGGCCAGAAAGACTTCC AGGGAACCTCATTCAGGAGGTGAAATGATGATGACTCCTCCAAGATGAAAA
WI-19201	179	T C ---			GCAGTCTTAAGGACCCTGGCCATTAGCTCTTGCTTTTGATGGCATTCTTTCCACCTTGCTCTCTC CTTGCTCTCTGTGTAGTGGCAGGTATGACAACTCATCCAGTGGAAACACAGCCTCACACTGCC CTTCCGCCCCCACACTTTCCTGCGAGGTGACCCGAAGGACTCTGGGGGATAAATTCAAAAA GTGTGATGTCTGCTCAGAAAGTCAGACTCCATGTCTGCTTGGCCTCAA
WI-19034	45	T C ---			GAAATGGCTCCACTCAGAGCTACCCGGTGATGAGGATAGGGGAATCTCCTCTTATACATTAAAG GCAACAGCAGTTAGTAAAGGTTTTACAGTGTCTGCTGTTTGAAGTGAATATAAATTTTTTG CTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTCAGCATTAAAGTCTGTGCAATTGAC ATTGCTACTTATAAATAGTCCCTAAGTCTTCTTATGCTGCTATATA
WI-19102	25	C G ---			TGTTCTGAGTCACGCTGAGGAGAGCTGCTTCACTCAGGAGTTCATGCTGAGATGATGATGATTCA TGCGACGTATATTTCCCTTTGGAAACAGAAATGAAGCAGAGGAACTCTTAATACTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAGTCTAGAACTCCTGTAAAGTTTGAACCTCAAGGAGAGGTAT AGTGAATGAGTGTGAGCATCGGGCTTTGCAAGTCCCATAGAACAGAAATGGG
WI-18548b	65	A G ---			AAAGGAGGGAGAAATCTTTTACATAAATGCCCTTGATCATCTCCAGTCCCTCCTGCTGGGAA[A G]AAAAAGCATCTNTCAAGTCTTTGTCCTTGGCTGC
WI-18548a	62	G A ---			AAAGGAGGGAGAAATCTTTTACATAAATGCCCTTGATCATCTCCAGTCCCTCCTGCTGGG[G/A]A AAAAAAGCATCTNTCAAGTCTTTGTCCTTGGCTGC
WI-18700	97	T C ---			GGCAGCAGCTTTTAAATTTGAACACTTCTCTTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTTT[C]AAGATCCACAATTGCAAGGCCACTGCTGGCTCA CTTCTCTACA
WI-18501	121	C T ---			CAGAGGGAAAGTTTATTGAGTCAGCCACAGAGGAACAGAGAAACAGACACAAGGAGGTTCTGTGT GCATGGAGGAAATCAGGGCGCGNACAGCTGAACCTCGCGCAGGACAGAGGGGG[C/T]GGACAGCA GCGCATGCCACAAACATTCA

WI-18017	87 C A ---			ACAAAGAAAAATGGAATAGGTTTGGAAAACTTATCTGCTGATGACAAAGTAATCCCGTAGATAA GGAGAGGCAACCCNGGAACA/C/AJACTGCTGGATAAATCGTTTCAATTAATATATCTCTTTGCAT CAGAGCTGGTGAATCAT
WI-18148b	101 A G ---			TTATTGGTTCCTTCGATAAACCCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAAACGAAAGCA GTGATTTCCAGAAACNCGATTCTGAATATCCG/AJGTGGCGGCATATGCAAGGAAGATGA
WI-18254	64 T C ---			TATACGGATCATGTATTGTGTGACCAACCACCTACACAGTCAATTTGTAGAGCAGTTAAATCAC/T/C JGCCAAATCCCTCTTGCTTCCTTGTAGTCAGTCCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCGGTTCCTAGACATTT
WI-18265b	117 C A ---			CAAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAAAGACGGCTTCTGGCCNCTCTGCGTCC AAGGTGTAAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG/C/AJGTTTTCAACCTTTC CTGGGTGGTTCCTCAG
WI-18295	40 C T ---			ACCACACATTTGTTGAGAGCCCTATTGTGGAGAACAAACAG/C/TJTTGGGAAGTAAAGTTGATTACT TCCTCTCCAAGGATGATATGTTAATGAATCCCTTNCCTTAGCTTCACTTTCATAATGCCAAA
WI-18459b	64 T C ---			GGGCAAGAGACAGAGATTTAATTGAATAAAACTCCAGGCTGTGACACGGGTGGGAGACACAAAT/ CJGAGTAATTAACAACATAATATTTANATGACAGTGAATTAATAACGTCCTGGGTAAAGCCAGAG GGGAGAGGGCGCTTTC
WI-22585	56 A G ---			TTTATTTTAAATTTGCATCCTGAGATAATAAAATTTATCTGACAAAGTGAACAATG/AJG/CAGAAAGC AGCAGTGAAGTTTCGGAGAGGAGGATGCTTCAATTTGGACAGCTGTATATAGATTGA
WI-21155	36 A G ---			GGGCTGTGGAGTAACAGAACTTGATGGAAATTTGGC/AJGJCTGTGTAGAATGATTTCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88 G A ---			GCCTTGTCTTTGCTGCTCAGAGGCCCTCAGATGGATACGACGCACTTCTTTGAACCTTTTAT TTTCTGGCAGGAAGAAG/AJGGATCCAGCAGTGAGATCAGGAGGTTCTGTGTTGCACAGACAG GGAAACAGGC
WI-19888a	98 C T ---			GGCAGGATTCACCCATAACAGAGAAATACTCCTTATTGGAAACAAGGTTTATTTTGATATGATG AAAATATTTTGGAACTAGAAAGTAGCAGTGA/CJTTGGACAAACGTTGTAAGATATTAATGCCACT GAACCTGTTCAATTTAAATGGTAATTTTCATGTTATGTGTTATTCACCTCAATTAAGAATGGAACATGT CTTATAATTGTAATTTACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82 C T ---			TGAGACCATCCTCCTCAACAAAGAAATCAGTCAGTTCAGCACCTAATTTTCCACACTGAAGTCTACG CAATTTTCATGCAG/CJTTGTGCACACAGTACAGTGCACAAAATCCAGAGGGCAACACATTTGTAATT CATATCATCGGTTTCCAAA
WI-20601a	125 T C ---			TCAGAAATGCTTTCCACTGCCCCCAACCAAGAAATTTAATGAATGONCTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCCTTGGAGGTTGATGACAGGATTAGTCTCTGTGTT/CJCTTGGT GCAAGTTTGAACCAGTGATTATGTACCATTGCATCAGAGCATCTGTTTCCCTGTGATGCCACCTAG

WI- 20561b	94 T C ---	---	---	CGTTGCTTATTAAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATTATG TACTTCAGATGAAAAATCCTTACATGTC/C/GGAATCAATGTCTTTTAAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20561a	25 A G ---	---	---	CGTTGCTTATTAAAGATGGCTGTTT[A/G]TAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCAATTA TTGACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAAAATTCAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20116e	69 T A ---	---	---	GCTTTCATTTCTGTACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAACAT AT/A]ATAAATCTATATCATATATTTATACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116c	59 T A ---	---	---	GCTTTCATTTCTGTACCCACCCCTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTT[A/J]TAGAA CATATATAATCTATATCATATATTTATACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116a	22 C G ---	---	---	GCTTTCATTTCTGTACCCAC/C/GTGTCCACCAGTTATGTTGGCCTTCAATATATGGCGTTAGAA CATATATAATCTATATCATATATTTATACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGCTCTCCCATGCCACTTAAAAATGNGCACAGGTTTGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20466b	133 G A ---	---	---	AAAGATTGCAGTCTGGGACACAGTTTGGAAAACACTATTTATAAGTTGGCCATATACAAACAG NTCCCAAATGGTGAAACTGGTATTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGC G/AJTGGAACATAATGTTTAAAAAGTTAGAGCTTGTCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTTCTTTGCTCTTTTATCCCTTTCAGGTTTCGATT
WI- 21444	39 A G ---	---	---	CTGGCAGCAAGTAACCAATTTTAAAGAAATAGTCTCAAC[A/G]AGTTCTTTTATGCGGTTATTTCA GTTGTTAACAAAGTTAAATACCTATTGGAACATAATCTTTTGTATTATTCGAGGAAGAAGAACTCT ATAAGATTGACTTACTCATTGTTGACTGGTTTGAAGCCTTACTGGG
WI- 21034b	148 T C ---	---	---	AGAATGGACAATGATGAGATGATTGTGAGCATTTTGTAGAAAGTGGTATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAATTACTGGTCATGG GAGATTGGATAGA/T/C/GCCTAACCTATCTCAATTTTAAGTAATGTGAGCAA
WI- 22091c	205 G A ---	---	---	GGCGTATTGATGCAATGTCCACCAGTCAAGCTATCATTTGAAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCAATGTAAACATACAGCATATTTACCTCCCCCTTAAGTACTCAATTTTC ATTACTTGTGTAGCTTTTAAAGGTTTAAAAATGTGAGCATTAAGTGGTATTACTTGAGGGCA ACA[G/A]AATACGGCTTAACAACACACACTAAATCATGAGGCTCAGGGATTG

WI- 21805a	45 A T ---			CAACTGCTGAGGCTTTCTACAGTGAATTTATAATCCTATATT[AT]AAAAAAAAATCTATAGTCTG CAGTCTTTGACATACCTTCTCAAGGGTGGATATGTTGGTGAATGCAGACTCCATCAATATGTGTGGTT TTGTTTGCTTTTGTAGCTTAAGTCTGTTAGNAAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATCGAACAGTTGAAGGCTGTTTGTGTAATTGCTG
WI- 21778b	155 T C ---			AAAAATCCATAATATTGAAACCCAAAGTTACAGAGAAAGTTTCGTAACCTTTTATTGAATTTATGAC TCTGCCCGCTGTCGTCGCTTCACTCCAGTCTGTCATGCCCTGTGTAGGTGGGTCCCCCAG GTCTGGGCTTCTGAGGTCTGTCGGTAGAAGGAGGGCAGGTTGGT
WI-20907	241 A C ---			TGAGTCAGTGTGATGAGGCGAGTTCGCTCAGCTGCAGTCCCTGACTCCGGAACACTGTGCTCT CAAATGATCTAGAGCTCATCTTGGGCGTACATGAGGGCAGTTGTTGTTCTAGTACCCATTAGCCC ATGGCTCTCAAGCCAATTCACACTGGGAAAAACACACCTCACAAGATGCCATCCATTGAGTTT ATACAGGTTTGTAGCTAGAACTAAAAAACATTTTAA[C]AATATCTA
WI- 21449b	222 C T ---			AACAGCAGCAGTCACTTCCAAATGCAAAAAAATACAAATTTTGAATAAAATTAATGTTTA TAATGCGGGTCAGAAGANTTGAAGGTACAACAGAAATCAATCAGCGCACTGGAGGCGCTGGAG AAGCCAAAGCCCACTGTGTCAGGGTCCAAAGCTGACAAGAAGTCCCAACCTGAGAGGTCTCCACACC AAATCATACCCCTCAGCTTCCCA[C]TTTGACAGAGCCAGTGTCTCTGGGTTAG
WI- 21558a	157 G A ---			GCCTACAAAGGAAGCCTGTGGACAGCGAGTGGTGGAAACCGACTCCAGCTGGAAAAACCTGCCCTC CCATCCCCCTTAGCGCCTTCTGGCCTTCCGGCTGATTTCTTCGACAGAGTTCTGCCAGGGCAAGG AGCTGTGGTGGGGGGCAGTATG[A]AGCCAGGGACTCCCTCCACACAGATGAGGCCCTAGGGGCTGCAA AAGGGCCCCGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI- 22187b	178 G A ---			TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCCGTGGCTAGCAGAGCTCATGGNGACCA GTCCTGGCCCTGACCAATGGGTGATTACATTTAAAAACCAAAACCAAAACAAAAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGT[G]A/AAATTTTCATGAAAAATTTCC CCTAAACCATAAACAAAACACTGTCTCTCTACCCCAAAAGTGTGGAGGAAAG
WI- 22187a	110 C A ---			TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGGCCGTGGCTAGCAGAGCTCATGGNGACCA GTCCTGGCCCTGACCAATGGGTGATTACATTTAAAAACCAAA[C]A/CAAAACAAAAATACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGGAAATTTTCATGAAAAATTTCC CCTAAACCATAAACAAAACACTGTCTCTCTACCCCAAAAGTGTGGAGGAAAG
WI- 21609b	146 G A ---			TCATGAATATGAGCCTCCATAATCTTCTCCCTTGTACAAACGTGCAGTCCGTTACAAAGCTGTAAA AACAAAGCCCCAACCAAGACATCACAAGAGGCAAGAGCAGTGGCAGTGAGAAGGGAGCCTGTAAAG GATGTTTCAAG[G]A/JAGGGTCCCGGCTATGTGGCCCACTGGATGTAGGCAGTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---	---	---	TCATGAATATGCAGCCTCCATAATCTCTCCCTTGTAACAAJCTJGTGCAGTCCGTTTCAACAGCTGT AAAAAAGCCCCAAACCAAGACATCACAAGAGGCAAGAGCAGTGGCAGTGAAGAGGGAGCCTGT AAGGATGTTTCAAGAGGGTCCCGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG
WI- 22512a	104 T G ---	---	---	ACATTCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAATCCCTTGGTGCCTCCCTAGGGCTTCA GGGTAAGCCCTGACATCATGGTCTTTGTGATCTGT/GJACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCCAAGTCTAAGGGCAGGCTACACTTGACTGCA
WI- 21028b	139 A G ---	---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGGATATGTACAGGGG TTTCJ/GJTGCACTGGTACAGAACACACAGGGAGTTTCACAAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---	---	---	ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAAATTTCTGCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGGJ/CJTATGTGACAG GGGTTTCATGCACCTGGTACAGAACACACAGGGAGTTTCACAAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---	---	---	ACAACTGCCTGTTACAGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTGJ/GJTTTCA TCATACAAGACAAAGCACAAAAGCACCCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI- 18829b	35 T A ---	---	---	ACAACTGCCTGTTACAGGGGGAAAAATCCTAGGTT/AJAATAACTTATGTGTACTTCTTGATTCA TCATACAAGACAAAGCACAAAAGCACCCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---	---	---	AGCCAACTCAAGGCCAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGAAGCAAGGA GCACAGGTAGTCCACAGAATA/GJAGACACAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTAA AAGAATACTAAGATTAGATGAACACAACTCAGAAATACTCTAGGAGAGCTGAAAAAAGAAAGGAAC AGATGTTAACAAAAACAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---	---	---	CTCTGAACTAAAGGGCCGTGAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCAIT/AJACAT TGGCTGGAATGAGGTGGTCAGGAAAAATAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAGTGAATAATTACAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTCTCCCTTAGGAGATGAGGAGTATGGGCCITAGGT
WI- 22130b	165 C T ---	---	---	TGTTTTGAGGGCTGTAGCAGACTACATAATGAGCGGTGAAGCGGCTGCCCTTCCCTCTCTCTGACAC CAGCAAGGGGGAGGCCACCATCACCGGCCCTGCCCATCATGCATCCAAATGATTACTAGCTAGGAA GCCAACGGAANAGACCCCGCGCTTGCJTGJTGTTTAAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTGATGGGAATGAC

WI-21661	117	G C ---	---	GCTTAGTCTCCACCCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGTCTTTCCAACTTTAGAATGTATAAATAAGAAATGACATTTTAAAAATAAATAA(G/C)TTTAGTCACAGTCAACAAAACTACCTTCTAAGGAAAACTGTCCAGTGAAGCCGTTAAATTTGTGCTTTTACGCTATGAAG
WI-21980a	25	T C ---	---	GA TCAGTTAAACACATTCATCAAGGAT(C)JAGATTAAATTAATGTCAAGGTGAGCATAAAAGGGAGATTATAAACAGAAATGTGTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTATTAAATTTTCATGGTGAAGCCCTGGGATAAAG
WI-21636	71	A G ---	---	TGCTTGTATTAAATGTGGTGTACATTATCCTATTTCACAGATGGAACAGAAAAATACCAGCTTTTGTAAJ/GJTAGCAATATCTATTATTATAATAAATTGAAATAACACCATATAATAATACATAAGGAAGTAATCTAATTGTGTTGATTTTGCAGAGGGGAGAAAAACATTACCTCTAGAGCTGAGGCTATTGTGCTCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGACAGGGATTTC
WI-22457a	112	G A ---	---	TTGCTATAATTTCCTTAAAAATGCAAAGAGTACATCACAGCAGAGTATAGCCAAATCACTCATTAGACAAACAGTAACATACCTGGACACGGTTTCAGGCATGAAGGATACA(G/A)CAGTTAATTAACATAAAGGAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAAATACCTGGGGCCAAAACCACTGAACCTACCCACAGCTGAAACACATGAAGGATACCTGGGTAAAGGA
WI-21524b	97	C T ---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGTACGACCTTCGCGTCATACTTAATGGTTAATAACAGCATTCCTGTCTACCCCGATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTCCGACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTGCAAAAGATTCTTGACTTCTCCAAAGTTACTTCTCCAGGGGATG
WI-21524a	35	A C ---	---	GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATJ/CJGCCGTGATGTACGACCTTCGCGTCATACTATAATGGTTAATAACAGCATTCCTGTCTACCCCGATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTCCGACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTGCAAAAGATTCTTGACTTCTCCAAAGTTACTTCTCCAGGGGATG
WI-22652a	32	G T ---	---	TTACCTTCCAAAACCCAGGCCACTTTGGAGAAAG(G/J)AAGAGAAATGCTATTAAATCAATAAGCCAAAGACAATAGGGACTACCTGGGGTAGACCAAGATGGGCAGTCACCATACACCATCATCTCTGCCACAGAACCCTTGGCACATGCTGCCCTCCCTACTCCGCACTCACCTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTTCTTTAGGG
WI-21703d	197	A G ---	---	CAACAGGCTCATGGAACAGAGCCCTAGGGATCCAGGAGCATAGGAGTGGTGGTCTGGGAGGGGCTCTGCATCCCTTTCTCAGCACAGACCATCTTACCCCTCCTGGGAAAGCAGCATTTGGAGCCTACACCACTTGTGCTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAJ/GJGTGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAATCTGTGGGGGAAGAG

WI-22724	117 A G ---	---	---	TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGAAGTGTAGAGATATAGGA CAAAATCAAGATTGTCAAAATGTATAGTAAGCTGTTAAAGCTTGCTAAGGGT[A/G]TATTCTATTTT TGGGATATGTTTGGGAAT
WI-22750	48 G A ---	---	---	TGTAACCTGTGTTTCTGAAAGTTGAGGAAAGCTGAGGCAGCTAATG[A/G]GCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATCTGACCATCTGACTGTGCT
WI-2275a	60 A G ---	---	---	TGCTGTTCTTTAGTTTCATGACGTTTATCAAAATGTGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGAATAAACTCCCTAAGGGCAGCAATAATTTCTGCTTTGAATCCTTCATTCAGGCCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAACCTGAGGTATGAGGTGTTGGGAGCCAGGAAAGGAAG GGT
WI-22808	143 C T ---	---	---	CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAAGTCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAGAGAGTAGGTATAAGAACCCAGGAGAGTGGGGTCCAAAT ATC
WI-21016	207 G A ---	---	---	TCCTCGTGTCTTGAGCCCTCATCCCAACCCCTCCAAGCCCTCATGCCACACACACCGTGTCACATTT CCCCATCCTCCCTGTCTGCCATCTCAAGTCCAAATCCAAAGCCAGAGCCCTGGCAGCTTTCTG GGAGACAGATGAAAGGAGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGGCTGTGGGTC CT[G/A]TTGGCGTGGTGAITGGGGGCCAATCCTGAGGCCAGAGTTCA
WI-21031	31 C T ---	---	---	TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTCTGGTCCCAATTTGCTCCAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122 A T ---	---	---	CCATATCCAGTCTCTTTGAAGCTTTCTATTGACITTTAGGGTCAGTTATTATATCCTTTATCACTAT GACTTTCATTTGATTTTATTTGTTCTTCCATTTCTCTGTCAACITTTCT[A/T]TTTGTATTATAA ACTGTTTCTAAACITTCACCTTAATCTCTATCTGTATTNCTGTAGTCCCTGAACITCTTTTAGAGG
WI-21186	95 G A ---	---	---	AGCGAGCATCAGAAATCAGCTAGAGGGTTGACTAAACAGACTTCTGGACCCACCCCCAGAGCTTCT GATTCAGTAGGCTGAGGTGGGCTTAC[G/A]AATTAGTATTCGAAGACCTTCCTAAGTGTGCAG ATGCTGCTTGTCCGGGGAACACACTTTGAGAACTATTGTTCTAAAATGTTCTCTCTCTTTTAA GGAGAGACAGGAATCCAGAGAAACITGCTAATTTAAGCATAATGTATTGAAT
WI-21187a	94 A G ---	---	---	CCACGATAACTATAAAGCAGAAAAATTAGCTTTGAAATCAATAACATAATTAGTAACACACATT CATTTTATAACACACATAAAGACACC[A/G]GGNCTCAGTAATGCTCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCAATTTGCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACCTCTGAGGGGTGAGACCAAGCAACCTGT

WI-21190	39 T C ---	---	---	TTTTCCCATACCAATGCACCTGTTGTATAACTATT/CJGTGGGGTAAGCCCTCTTTGGAGAC CAGTGACATAGACATGATCCCATATTATTAACAATAATTAATAATCTGTACTATTACTGC TTAGTTATCTAGTGTATTGAGAAAGGAGAGTCAGCATAGTTATTTCCATGTAATAAAGCTT AACACA
WI-19937d	186 G A ---	---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGGAAGGAAA GAACTATTGCACAACCAACATTTACATATCTGATTTAGACAAGCAAAAGCAGCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTTGGTGTGTTCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAGAAGCAGTCATTGAAAATGCTGACTTATGCAATGGCTCAGGAAGAA
WI-19937c	185 C T ---	---	---	ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAACTTGGAAGGAAA GAACTATTGCACAACCAACATTTACATATCTGATTTAGACAAGCAAAAGCAGCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTTGGTGTGTTCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAGAAGCAGTCATTGAAAATGCTGACTTATGCAATGGCTCAGGAAGAA
WI-21117b	227 C T ---	---	---	GAAACGGGGTGCTAAACAAAGAAAGTCTCAGATCCCACTGAAATCTGTTGAGTTTCACAGGCTC TCTCCAGAAAATGCATATGTACCAATTTGCATGTACAATTTAGAGCCTTCAAAATACATTTCTGGGG TCCAATCACATCTTCAGGTTGAGACTCCTAGCTCCCAATATTCACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGATT[C/T]TCTACTGAATCTTGGTGGGAG
WI-21122a	42 C T ---	---	---	TCACCTTTGATCATAATCCCTGTAAAGCTAAAGTTATCA[C/T]TAACAGGAACCTCTGTTTTCC TTATTCAAATGTACAAGCCTGACGCTTACTGTACATATTGCTAGCAGGAGACAACCTGGAAATACT AAACAAATCTGGAATTCACATTTACAGACAGACGAAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTGTTGGGTTGCT
WI-21254	53 A G ---	---	---	CAGTTTGGTACAGGAAGGGCCCATGAATGTGGCGGGAACCTATCCACAGGAG[A/G]CAAGGAGAAG CTGTTCTCTGG
WI-21054	23 G T ---	---	---	AAGGAACTGCATGGGTACAAAT[G/T]TCCAATTCATACTTAACAAGGTGGGAAACGGGTCAATTCT TGGCCTGCTCCAGAACAGGGGCGAGTCTATGCACCTCTG
WI-21059b	181 T C ---	---	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACCTCACTGAAGTCATTTCTCTATT[C/T]ATTTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGGCCTAAT
WI-21059a	63 C T ---	---	---	GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCACTGAGCCTGG[C/T] GAACTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAGACATACCTCACTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGGCCTAAT

WI-20442	37 T C ---			---	TCCACGTGAAGGAAGAAAAAANGGGGGGGGCTT/CJTAAAGGTGGCACAATTTTAAAGAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAACACAAAAGTGCAAGTGATGAGACGAA CA
WI-21235	43 T C ---			---	GTGCAAGAGGTGAAGCAAGGGACAAGGGCAGCAGGGCAGT/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57 T C ---			---	ATCAGAACTGCAATCTGCACATGAAAAGACCTGGGGGAATGCCTACATCTGGAATTT/CJCATTTAC ATCAACGTTAAATTTGTCCGACCAGTCTTCATTGCTGATCATTGATAATGACAGATCCAAACAT GAACTCCTGAAGCAAAATGAATATTACCTTGCTTTTCATGCAAAATTTAGGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACCAAGATCTAAGGAATTTGTGACAGGGATCTTCT
WI-21149a	167 G A ---			---	AGGACCTGCTCTCACACGTTCCCTACCCCCACCAGCTTTTGGCAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTTTTTTTTTAAACAATGACCTTATTTTATCTTTTAACTTAACTGAGTCTTATATA CAGACCTGCCCAACTGGAAAGCTTTTACAC/GAJTGCTTCAGAAATGCGGCAGTATGACACAATGGTT TGGGGCAGGTTCTGTGGTTAAACATGGGATGGAACCCAGGCTCTACCTG
WI-21376b	188 A G ---			---	GGTGCAACTTGGAAATAATGGTTTAAAAACAGGATAAGCATTAAAGGAAAAACACTTCAATGTGTC TTCCATTTGATGAATTTGTTTTTCTCTCTTTATCCCGCAAGTGAGTTTCATGCTCGGTGAAACCA GACAGTGAATCTGTTCCAGCCCCAAATCTGCAGCATTAGGGATGAGTCTC/A/GJGAAAGTGATTCT GAACTGAGCAGCACTCATGTCTGCATGGGAACCTCTGGGGAGAGAGCCT
WI-21382d	125 C G ---			---	CCATTGCAGTCCAGAGATGAGAACTGGACCAGAGGCAATCATGAACAGAACGGGAGTCAAGAGA AGGGGTTTCTAAGATGAGAAAGTGGGGGGGTTGGATCCAGTGGGATNGGCTTCC/CJGJAGGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCAGTCTGATGGGGAGCAGAAAGAGTGCCTCATCCTC AGTCAGGTCGAGTCAGGTCGAGGAGAGCTGCTGCTCATAGTCTCGCAC
WI-21437a	201 G A ---			---	TCCTGAGGTTGGAGTCTAGCATAGCTCCCTCCCTCAAGAGGACAAGGGTCAGGGGCGAGAGC AAAAATCCAGTCTGCTCAACCAAGGAGACTGCTTTGGGATGGAAGTTTCTGGAGCTCCCTCCAT CTATTCTGTGGGAGGAAACATGCCAGGGCTGCTGGTAAATGGCAGGGTCACTTTACCAAGGGGQ/G /AJCAGGCATAGTGTGGCCCTGCTGCTGCTGGGGCCACCTGGGAACAGT
WI-21202b	156 A C ---			---	CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGT/CJTGA GTTTTATGAACATGATTTTATAAAAATGGTCACATATATTTTTTAAAGTTAACTGATTTATGA AGGAGGAGAGAGATTGACCAAJA/CJGTCTACATGCATAGACAGTCTCTAAAAGCGTATCTCAAAACATG A
WI-21202a	61 T C ---			---	CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGT/CJTGA TCTGTTTTATGAACATGATTTTATAAAAATGGTCACATATATTTTTTAAAGTTAACTGATTTATGA GGGAGGAGGAGAGATTGACCAAGTCTACATGCATAGACAGTCTCTAAAAGCGTATCTCAAAACATG A

WI-21627b	153 A G ---	---	GCATGAAAGAACTCCAAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAAJ/GJTCCAAAGTCATCTAATATTAAACCATATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21627a	106 A G ---	---	GCATGAAAGAACTCCAAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCJ/GJTTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATTAAACCATATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAATAAGGGTTTAAAAATGTTGCTTA
WI-21399a	75 C T ---	---	GGATTTGAGTCCCAACTTGATCTCAAAATTCACCTTCTTGCAATGTAACAAGCTCATTCCTCTAAAGTT TCAGTTTJ/TJTTACCAAGTAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATGCTTGGTAA CTGCCTCTGCAATTTGCTCTGAGGTTGTGTCCCTAGGACTAGGTAGGATCTCTCTGCTTCTGCC TTACCTAGGCATAGTGCTGATAGCAGGCTGAAGCCCCAATTCATCTGT
WI-20329a	68 G A ---	---	CGATGCTGCTAAGATAGGAGGTTAAATCTTTACATGGTGGTGCACAGACAGACATCAAT CJ/GJTCGTGTAGCAGCGAGAGACACTTTAAGTTGCCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTCTGGCTTCTTAAAAACAGTAAACCAATCAAAAAGAAAGATTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACACAGAGCCCTTGAAAGGAAAGGCCCTCACT
WI-21249	155 T C ---	---	TTCTGGCATCAATGTACATGTAATAATCCAATTTAACAGATCAAAATGTTACACTAAGTTTCAC TAGTATCTAAGTATCCAATCACAATTGTATCTAAGTTTCACCTTTAAGAAACATTATAAAGGTAATT AAACTCTAGGTGTATCTTATJ/CJATGGAACTAGTTTATTCNNATTTAACTACTGTTTCATTGGGTA AAGTATGTTGCCCAATTTTCAGCTGTTTAAAGGAATTTATAAACACATTGAGA
WI-21504	147 C T ---	---	TGACACAGCATCAATTTTCATGAATACCTTTGAAGGGCCATTAGAAAAAATAAGAGCCAAATTTGGGTC ATTTGAGAAACATTTTCAGCAATACAGTGGGGGCACGGGCCGTTCCGCTCCAGCTGGGTTTCCC AGATGCAACAATJ/CJTGCGGTTCTGGCTTCTCCACTGGTGGGATCGCGCCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---	---	CTGCACAGGGAGGACAGCTGCTGGCAGGGACTAATAAACCTTCCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAAACGCGGGCAGGGAGGGGCAGAGAACJ/GJ/CACATAGCTTGGGGTG GGCACCAGCTTCAGACCCCTT
WI-21475c	181 A G ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGCTGGGTGGACGTGGCCCTGATGTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTGCAACCCAGGCTTCTCACTTCTTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGACAGTGCCTTTTGGAGAAAGGCAJ/GJAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCGCTTCTCCACCCTATTCTCTCCCTGAAAG

WI-21475b	117 A T ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGCTCCAAACCCAGGCTTCTG A TCTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGCAGTGGCTTTGGAGAAGGCCAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTCCCGTTCTCCACCCTATTCTCCCTGGAAG
WI-20893d	207 A G ---	---	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCGTTGTCAGGCTTGTCTGCAGGG CTGTCTTCGGCGTTTAAAGTCTACTGAGGAATACAAATCATTTGTACGTAAAGTTACATCCGCACTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGCAGT TTC A GIACATAACATTGGTAGAGTAAACAACAACCAACCAAGCCTAAATG
WI-20893c	179 T C ---	---	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCGTTGTCAGGCTTGTCTGCAGGG CTGTCTTCGGCGTTTAAAGTCTACTGAGGAATACAAATCATTTGTACGTAAAGTTACATCCGCACTCC AGCGTCAGGCCAAACCTTCCGTGGACCTGGGNAACCTGCCATTTCTCTCTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAAACAACAACCAACCAAGCCTAAATG
WI-19941c	71 C G ---	---	GAGCTCAAGGGAAGACCCCTTACCCAGATAGGACTAACTGGAGGGTGGAGGGAACCAAGGTGAAA GGTATTC G GGTCTGTTGAGACAAAAGCAGGGGGCTGAGAACACAGACAGCAAGGTGGTTGGAG GGACACAGAGGGTGCAGGAAGGAGATGGGGACATTTCTTATCCAGTGCATGCCCTTAAAT AACTGGGTACAGGAGCATTTTGAAGGAGAACCAAGGACAGACAGCAAGGCG
WI-21552b	166 C A ---	---	TGGGTACATGGACAGATGATATGTTTATGGGTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAAATCGGATCTCTTCACTCAAGCATTTATCCATAGTGTACAAAGAA TCCAAGTATACTCTTGATTTATTTAAATGT C A AATTAATTTATTTGAAATTTAGTTACCCCA ATTGTGCTATCAAAATATTCATCTTATTCATCTTTGTAACATTTATTTGTA
WI-21552a	66 G A ---	---	TGGGTACATGGACAGATGATATGTTTATGGGTATATGAGATATTTGATACAGATACACAATGTG A TAATAATTACTTCAGAGTAAATCGGATCTCTTCACTCAAGCATTTATCCATAGTGTACAAAG AATCCAAGTATACTCTTGATTTATTTAAATGTACAAATTAATTTATTTGAAATTTAGTTACCCCA TTGTGCTATCAAAATATTCATCTTATTCATCTTTGTAACATTTATTTGTA
WI-21512	54 C G ---	---	TCCTCGTACTTCATGCTCCCTCCCTGCCACAGAACCTTACAAAATATTTCTGT C G TAGAGAGGGA AAGAGCTGGTCCCTGCTGAGGCAACGTCAGGTCGGGAAAGGCACCTCGTGGTCTGTGATCTGTC TCAGTATGGGAGGCTCTCCACTCGCCACAGGCGAGCTCGGGCCAGAGATGAGAAATATGCTGTAA TCCAGTACAGGGGCTGCTGTTGGGGTCCCAACAGCTCTCTTTGGGGG
WI-21513b	192 G A ---	---	CACATAGTTTCTCAAGAAGGATGAACCTGAAACCTCTTAAGCGAGCAACAAAGCAACTTTCCATT ATTCTTAGTTTAGACCAGAACTTTAAATTTATTTATTTCTCTTTAACTGTCAAAATACACCAATA CTTAGAGGAAATATTCACAGTATACCAAAACATTTTAAAGATAAAGAGGCGAGTGA G A AGTAG TATTCTACATACCACAGTATACAAATGATGCCCTTCTGCAAGGTTTAGGAAC

WI- 21514b	133 C T ---			TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAAGTATCTCAACATTACAAAACCCCAATCTTCAAGGAAGGACGACATTACCATGGAGC[C /T]ACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAATCTCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTGAITTTGTCAAGGGTCATAAGGAACT
WI- 21514a	100 A G ---			TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAAGTATCTCAACATTACAAAACCCCAJA/G]TCTTCAAGGAAGGAGGACACATTACCATGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAATCTCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTGAITTTGTCAAGGGTCATAAGGAACT
WI-22020	27 C G ---			ATGAACATGTTGCAGTGGGATGAATC/G]TTATCATGCTAAGTGAATAAGCCAGACACAAAA AATCCAATGTATCATTCTACCTGTATGAGGGTACTT
WI- 19576a	113 A G ---			TTCATCGGTTCTTAATACAGTACATCCTTTTGTGTAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATTG/A/G]TCTAGTTCAGTGATTAGT CACAGAAITTAACATCTGCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCCACGGGGA G
WI- 21695a	141 A C ---			ATACACAGGCCACAATTGCAGGATGGAAAGGCGAGTGGGCACCTTGGAAAGTGACTACACATGGCAATA AGCAGCCTATCTTCTTACCACCAAGAGTTCTTGGGCGATGTGATGGCCAGACCCCTTTCCAA GGGAATA/JC]TACTACACTAAGCCTACACTGTACTGTAGAGTCACTGGTGAACAAGGCCACAGGC AGTGGGAGGAATGTGATGACTTCACTGTGTTTCAGANTTCTAAGGCCACAGCAT
WI- 21574a	235 C T ---			AAACCCAGAAATTTAGGTACTTTTGTATTATGAGGAACCTCACTACTAGGAAGCAACTTATAGTG TGTAATATTGATCTAGCAGCAACTTCCACTGATCCTGGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTGTGAATGTCCTCAGAGTCACTAGGGAGCCATT GGGCAGGCCAGGGAACCTTACTGCTACTTCTTCTTCTGCTGTCAGGTGGGA
WI- 21644c	151 T A ---			TGACTGCCAAGATTTAGGCCCCAAGTTCAGGCAAGGGTCACCTCTAACCTTTCAGGAAGCTTGGGT GTGACCCACTGCATAAATGGATTTTCCACATANTATTACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGAT/J]TCAATCAAGATCCATGGAATGATGCAGTTTAAACATGTGTCTCAGC TTGCCTACTGACCACCTTCTTCTTCTAATATGGCAACAGCACAGCAAGTC
WI- 21614b	55 G A ---			TGCTTTAACCTCAAAAGTCCAAATAAACATATAGACATTTTGANTATAGCTATC[G/A]TTTTAACA AACCTCATATGATCACTGTGCAATTTTCAGTCACTAAATACGGAACCATGACTATTATAAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAACCATACGTGTATTTCTAAGGTACTAGGGAGTT GGAACAGCTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI- 21615b	151 C T ---			GACCGAGAAAACTGCAAGGCATATGATGTTTGTGCAAGTATCACATGACTATTTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAGATGGCTATTTTAAATTTACATACATATTAAGATAAGGATGGACT CTTTCACCTGAGTATTATC/T]AGGACACAATCGCGGATGTAATCTATTTGANTTATACCATAGGCCC TATCTATATTGGGCCAAAGGGAAGGTAGGATGGGTACTGTGGAAACGGA

WI-21981	61 T A ---	---	TGTCATCTCATTTCTGGAGAAATCATAGATGTGGCAGAAATACATATTTCTTGAAGAAAAAAATTA/JGTCTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAAGTACATGACAACATGCATGGGATAGA CACTCTGTTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGAGGCGTTTAAAGTTAAATTTGG
WI-21660	120 C T ---	---	TCCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGTGTAAACACGCCCTCTCCACTGCT TACTGTGTGTACCAAGAGGAGCAAGAGCTCACCCAAGCCTAACCTGGCC[C/T]TGCTCTTTTTCAG GCTTCTCAGGATGCCACAGCACATACTGGGGAAGTGGGATGCAGGAGAGCCAGGGTCTGTCTTC AGGAGGGTCACAGC
WI-19105c	211 C T ---	---	TGGAAGTAGCCCTCTGGACAGAAAGAAATATTTGTGTCCATGTGGTTGAGTCTGTAAAGAAGGA CACTAAGGCACATGGCTGGTGATCTTTCGCTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCTT GTCTGATGGTTCCAGGGCTGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCAGTGATCTCCCC ACAACT[C/T]TCCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCC
WI-19105a	33 T C ---	---	TGGAAGTAGCCCTCTGGACAGAAAGAAATATTT/CJGTGGTCCATGTGGTTGAGTCTGTAAAGAA GGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTC CTGTCTGTAGGTTTCCAGGGTCCAGGGTGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCAGTGATCTC CCCACAACCTTCTCCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCC
WI-21760c	81 C A ---	---	CAACCTAGTCACTCTACTGATGCAATGATTTGGAGGTGCTCTCCTAGCTTTACAATAAGNGGAG GACCTCTGACTGCA[C/A]CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---	CAACCTAGTCACTCTACTGATGCAATGATTTGGAGGTGCTCTCCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCACCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---	TCTGCCATATTGTTCCAGCACCACTATTACTGTATTATTTCTCTTTGAGGAAACCCAGGNATTAAAG AAATCTGTTTGAATTTCCATGATGCCCTAACTATGTTAAATAATCCTTTCTTACCCAAAAGGA ACTTCTTAATCACAGAGAAACAGAGGGGAAGACTGAGATATGTTGCAGAAATTTATCTCTAC[T/C] AGAGACAATTCATAGTTCATAATCTTTCAGGGTGTGCTTTACTTGGGGGC
WI-20934a	72 T G ---	---	CCAACATGCAACATAGTCTTCAATTTCTTAAAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCA GAGAA[T/G]TCTAAGACAAATGGTCAAAATATTCAAATGGCCTGGCAGTGTGGTAATTCAGCAGAC AAACAGCATGAGAAAGGGCCGGGAGACAGTAATAATACGTGCCCATTTGCAATGAGTTACCCAATC AAGCCCTTTACCTCCTTAAGATGGCAGATTAGAAGACCCTNTTCCCCAGGAGA
WI-21561	55 T G ---	---	TTTCCATTTTATTCAGCCGGGCCATCAGAACATAGCATCTATACCTTCGAAACCTT/GJCCTCTTAAC CTCTCCAGGCAAGGAAAGGAAAGTATGATCATATTTCCCTCAGAAATGGTGGGATCTCAAGACTT TTTAGAAAGTGTCTTAAAGTATAAGAGGCTTGAATATAATGATGATAAATGGTAGCCTTTCTGGA AATAAATTTTGTGTAATCTGTTTAAAAAGATTTTGGATGCATTGTCCCCA

WI-21961c	200 T G ---	---	---	AGCTTTGGCTTGAAATTTGGTACTTACTACCTTGCAATCTCTTATTATTATTATTACITTTATTT TTCCGTAAGTTATTGGGTACAGGAGGTTTGGTTATAGTTCTTAGTGGGATTTGTGATTT TTGGTGACCCATTACCAAGGAGTATACACTGCACCATACTCGGCTTTTATCCCTCGCCCC[T/G]C TCCCACITTTCCCTCAAGTCCCAAAAGTCCATTGTATCATTCTTATGC
WI-21961b	73 G A ---	---	---	AGCTTTGCTTGAAATTTGGTACTTACTACCTTGCAATCTCTTATTATTATTATTACITTTATTT TTCC[G/A]TAAGTTATTGGGTACAGGAGTATTGGTTATAGTTCTTTAGTGGGATTTGTGTG ATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATACTCGGCTTTTATCCCTCGCCCCCTC TCCCACITTTCCCTCAAGTCCCAAAAGTCCATTGTATCATTCTTATGC
WI-21956	26 T G ---	---	---	CCCACTTGGGTCTCTTTCAAGTGAATTT/GTTCCCTTCGTTCTTAAAGCCCTTTAAATGAAC TCCATTCCCTGTTCTGAACTTGCCTTAGTCTGTTTCTGCTTCATGCCCTCAGTCGAATTCCTTCTT CTGAGCGCGCAAGGACTGAAGTTGCTGTGGACCTGTAGGGTTCGACGCCGTTAACTCAGGGTAACTC CTATCTCTCCACCGGTAACAGAGGGTTACATTATGGGGTCCAGGTT
WI-21966	148 G A ---	---	---	CAACATACATTATGGTGCCTTTATTTAAGAAATGTTTACTGAGAATCTGTACTGTAAACAACATAT TTTTGTAGAAGCATGAGTGAGAGTGTGTGTGTGCGCGCGGCACGGCATGGCACTGAGG GGATTGCAATGGG[G/A]AACAGGATAAAAAGGTATAAAAACCTTGGTCCGAAATCTTTGCTTATTAAAC CTTGGCCCTGCTCCTCACAAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI-21930c	146 G C ---	---	---	TATACTGGTTTTGGTTACATGGATGAATTGCTAATGGTGAAGTCTGAGATTTTAGTGTACCCATCA CCTGAGTAGTGTACATTGTACCAACTGTAGGCTTTTATCCCTTACCCTACCTCCACCCCTCCCCAT TTTGAGTCT[G/C]CATAGTCCATTATATCACTCTGTATGCCCTTGCATACCCATAGCTTAACTCCC
WI-21139a	165 T C ---	---	---	GCTCTAGTGAAGAAATTCAGGACGGGTCTTCAGAGCAGAGGGCTTGGTCAAGTCCCTGTTCTGCCA CTTACTAACTGCATGACCTTGAGCAAGCCACTTAATTTCTCTGCTCCTTCTCTGTGAATGGGTACAA TGTGGGTGAGCAGTAAAGGAACATAACATACATACAGCACTTCAGCACAAAGCCTGGGCACACAG CACTGCATGGAATAACACAGGTAACTTTTAAACAGTGGGGACAAAATTTAAGTACGTGGCCAGC TGTTGGTTGCTTGTGGTCAATAAGACAAATGTTAAGANTCAGGAGTACTTAAGTGTAGTGGTTACA AAATTTGTTCTCTTCAGTTTTTCATTAAAGTAAATCTAATAGATATACATATTACTGCAGATAAA ACCATCATCAGAA[G/T]TATTAAATTAATGCATATTTTGGGCTACTCT
WI-20317b	217 G T ---	---	---	CAGGACTTGGTTTGTCTGCCAACTGCACATAAATGTCCTTTTGTGAGTTATTGGTTGTGCGG TTTTCTCTTTTGCATAAGAAATATGTCCATTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGGAGG GTACACGGGGCGTCCGCTCAGTTCGGCGGAAGGACGTATT[G/A]CTGAACCTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTTCAAATCCTCTTTGCTGCAACCTCT
WI-22082e	179 G A ---	---	---	

WI-22082b	67 C T ---	---	---	CAGGACTTGGTTTGCTGCCAACTGCACATAAAATGTCCTTTTGTGTTGAGTTATTTGGTTGTGTC /TGTTCCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTTGTCTTATCCGGATGACGG AGGTACACGGGGCTCGCTCAGTCCCGCGAAGGACGTATTCGCTGAAGTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTTCAAATCCTCTTTGTGCAACCTCT
WI-20993	139 A G ---	---	---	AACACAACTCCATGCTTTCAAGATCCCACACCCAGACTACTAAGACATATTAAAAATTTACAGCAAT TAAACAGTGTAGTTTGGTACATAACACATATAGCAATGATACAAATAGGGGAAAAAACCCCTGG GCTTCTT/GJTAACAAGTGAATACATTAAAGACAGTATTGCAGAAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCTATTTCAAGGCTTCCTAGCTCATCCACACATCACC
WI-21723b	125 A G ---	---	---	AAGCGATTTTATTAAATGATTTGGACATACTGTAGGTCAAATAATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTC/G/AJACATAAAATTTAGTACTTCAAAGGGTTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAACTCGGAAATC ATT
WI-21723a	82 G A ---	---	---	AAGCGATTTTATTAAATGATTTGGACATACTGTAGGTCAAATAATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTC/G/AJACATAAAATTTAGTACTTCAAAGGGTTAGTCATATTTCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAACTCGGAAATC ATT
WI-22132	99 T G ---	---	---	CAACAGATGCTTGAGCCAAAAAGCAACATAGGCAGAAATACAAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTTGCCTTTTACTATCCTTT/GJCCCAATTTCTTCTAATCTCTTTGCTTACAA TATATTACCTTCTAGGTATCACCTCATCCTATAGGAATGCCCTTCTAGTTTAAATGTCTGCCCCAAACA ATACTAACCCATTGAAGGATAACTATGGAACCTTTTAAATGGACAGTGGG
WI-21006a	106 A G ---	---	---	TGACAGATCACACCACATTTTGTGTAACTTTTCTCCTTCAAGAGTCACCTTAGCTTAAAGCCAGAA GATTCCTTAAAGAACACATACACACATGTGCACACAC/G/JAGAGGCAAGTACAAAATGTAACC CCACCAAGTGCATGTGAATGAAAGTGCAAAAAAGGCTTCATTTGCAAACTCTGAGGATCATTCTCT CTGCTTCAGGAAATAAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138 C G ---	---	---	CTGAGGCCTGCTCTAACTTCATNTGACGGAGCGAGTTTCTGCTTGGAAATAACTGAAAAGATTTCAT TTTCTCTTTGTGTACAAAGGATTCAAATAATTTTACATCTTCTCTGCGCAGTTAAACGTGCCGTGG CTC/G/JCAATACACACCAAGCCAAAGCGTAACTTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166 G A ---	---	---	AATGAAATGCCACCCAGAGGTTAACAGCTTCCATGCCATGCACTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGCAGCTTTGATTCCTCCATGAAATTAAGCTGTGTGCTCACTTGTTCATATAA CTCAGGCCACCCCTGAAATATCTGTAGTGGG/G/AJAAATTAACACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAAATAGGCATGGGCAAT

WI-21079a	50 G A ---	---	AATGAAATGCCACCAGAGGTTAACAGCTGCCATGCATGCAACTGTGT[G/A]CGCAAAATCAAGT TGTTTTAATACCAGTGTGCAGCTTGATTCCTCCATGAATTAAGCTGTGTGCTCACTGTGTTACA TAACAGGCCACCCTGAAATATCTGCTAGTGGGAAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI-22129a	45 T G ---	---	TCTGTAGATTTAGCCATGCCATATATTAACITTTAAGGAAAAGT[G/T]TATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTCAATAAGTTAGCTCTAACAGTTAAACATTGAAGTCTTATACCTTATATTA AATGTTTAGCAATCTCTACTACATTTTCAAATATAAATAATTTGGTGCAAAATCCAGNAAAGGGCA TTAACCAACATGGGACTGATCTGGGGCTTCCACCTGACTAAGGTTTAA
WI-21941	79 A G ---	---	TGGAGTTAAGTGGGGCTGCTATTTCCCCCAAGAGGACTCGGAAGATGTTGATTCAGGGCAGAGT GAGGGCAGAC/A/GJGGATGAGGCTCTTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGGTTGGGAGCCTCACCCAGAGAGCCTCACTGCATTGACCCACACCCACTCAOC CAGCACACAGGCACACGCGAGGGGCACACACACGNTGCACCTCACCCACGC
WI-18916b	42 C T ---	---	AATGGCATCCCTGTCGATACCAACATCTTCAGCAGCTCAGC[C/T]GGCTTCCCACITCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACCTGGACACAGCCTCAOC AATGCCACCTTCATA
WI-18916a	35 G C ---	---	AATGGCATCCCTGTCGATACCAACATCTTCAGCAGC[G/C]CTCAGCCGGCTTCCCACITCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACCTGGACACAGCCTCAOC AATGCCACCTTCATA
WI-19828c	200 A G ---	---	TTCCCTTCTCCCCAAGAAGTGGGCAGAAAAGCTTTGTAACTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTGTAGCCTAGTGCCAGGCTTCTGGCCCCAATTTCTGGTTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTCCTCTGACCCCTCACCACCCCAAAAT[A/G]CTTTTAACTCTGGAAAAGAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47 C T ---	---	CACAAGAGTCTGTACAACCTTAGGGACACAGCCCTGGCCCTGCCCT[C/T]AGCTGCATGCCACCCTC ATATCCACCCCATCCAGCCTCTCTGCCGACACCCCGAGCTCCCTGCTCTGGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCCTTGATCCAACCCACAGCATCT
WI-19860	51 C G ---	---	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAAGATG[C/G]CTGCATCAGTAT CTCCCATCCACATAATTTCTGTTGATTTTGCCATTACCCATAAAATGTTGGGATCTACCTCCCT CCTTGCAAAATTTGAGCTGNNCCTCTGATCTCTGCTAAGGATCTGAAGCC
WI-19889b	80 C T ---	---	ACCCAGCTCCTCTTACCCTCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAAACTGCAGGGCAAG AGGAGTGAGGGG[C/T]TACAGCAATTTATTTCCCTCTTTCACCTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATGTTCTTGGCCACAGTCGTAACATTGC

WI-19891c	172	C G	---			TGTTGGTCTGAGAAATTCACAGCTTACTACAAGGAAGCTGAGAAATTCGTTGGTGCCCCCTCCCCCCCGG ACTCCTCTGCTCTGGGAAACGTGGCTTGNCTCCAGACACGTGTAGATGCCAGCTCTCTCTCAGCGG AGTCCCGATCCCTCAATTTGCCATCTGTCTGACTC/GJGCTCTCCGGGGCGTGCGGCGTGTCTGT CAGCAGCGGGGGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81	C T	---			GCACCTGTAGGGGTGTAGCTTCCATGTTCTCCAAGCACGGGTGTACATTACCTTAGGCTGACCAT TCCCTTGGGGGG[C/T]GCAAAACTGCTTTGAGGAAATNTCCAGGAGGAATAAACTAGAAAGCGC ACCTGCTATTTCCACCATCTATGAGAAATACAGCTAATGAAGTGGTGGCAGAAGCTTGGCCGTGTGA GTGCCCCAGGGTAAAGTCTCTCTTCTGTCCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91	T G	---			AGCCATACAATGCATTGCAAGAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCGTCAAGTGTACAAT ACATTCATGTCCAGGATAAGGAGCA/T/GJACACCAGGATTTATACACGGTGGCAGCGGTATAGGCA CGATGATACAAATATAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGGAAGGATGCT GGGTGATCTTGTTCGCCGAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20270a	53	G A	---			AGCCATACAATGCATTGCAAGAAGAAACAAAGCAGCTGTACAGGAGTGGGACGC[G/A]TCAGTGTAC AATACATTCATGTCCAGGATAAGGAGCATACACAGGATTTATACAGGTGGCAGCGGTATAGGCA CGATGATACAAATATAAGTATATTTCCATCTATATAATACACAGCTGGGTGGGGAAGGATGCT GGGTGATCTTGTTCGCCGAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20622	130	T C	---			CCACTTCAATATTTACAAATGCTCAGCGAGCAAAATATGAAAAGCTTCAACACTTTCCCTTTTGTA ACTTGCTGCAATAAATGCAACTTTAACAAACATACAAATTTCTCTGTATCTTAAAGTTGAA[T/C] TACTAATTTTATGATGTTACTCATATTTTATTCATATACTTTAATGACATCATTTGCCAATACATA CATTATTTCTNTAACTTTATTTTACAATAAGCCCAACATCTGTCAATGCAG
WI-20768b	190	C T	---			TTCCTCACTAAAACCTCCACCCCAACCTTCTCTGGAAGGCGGGCTAACAGGACCTCTGCTGCTGCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATCTGTATATCACCACCTTA CAGGAGAGGTCTATTTCTGGGACCCAGAGNCTAGCAGACATCTGCTGGG[C/T]CAGGGGACTC GTAATTCGCTTGGTCCAACTCTCTCTATGGGGTTAGCTGCCCTCATTC
WI-20768a	71	C T	---			TTCCTCACTAAAACCTCCACCCCAACCTTCTCTGGAAGGCGGGCTAACAGGACCTCTGCTGCTGCTGC TCA[C/T]GACTGATTCTCAATCCAGCTGCAATGCAAACTGAAACTCAATCTGTATATCACCACCT CTACAGGAGAGGTCTATTTCTGGGACCCAGAGNCTAGCAGACATCTGCTGGGACCCAGGGACTC GTAATTCGCTTGGTCCAACTCTCTATGGGGTTAGCTGCCCTCATTC
WI-21909	153	A T	---			TGTTTGCTTTTGCCAGGTACTCTACTGCTTTACATAAAATATCTATTCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAATAAGGATATTGTTGTCATCTTTAAAGAAA TGTCTTAACATACCAAAG[A/T]AGTGGAAATCAATAGATAAAATATTTAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCACCTAAATTTATATTTCTATGTATGGAAG

WI-22202	128 A G ---				TGTTGCTTTGGTTGTTGCTTCTGGAACATATTGGAACACTTGTTTTTCATAAGCTGTCTGACAGT GGCACAAATCCCATCCATCTTCAGGCCTTTTAAAGGTCATTATGAAATCTGAATTTCTT[AG]TTAAT ACTCTGGTGCAATTCATCTGCAAAAGCAACTGGCACAACTCCTTGCCGGTGACGCTCTCGG AGAACATCTAATATTGAGTCTAGTTCTGTGGGAACTTCTCCAGCTCAC
WI-22189	70 C T ---				CCAAGGATGAAATTCACATTTATTTTNCCTTTATGTGAATAGAAATGGCAGTGAAGTGTCTCTATG AACTGAGGGAGGAATGGCATGGCGTGGCGTACCAGCTGGACGTTGTGCTTCCAAAGTACAC TATGTGGTGGAGACAAAGGGT
WI-22283	109 T C ---				GGGAGGCATCATAGAAAAACCCCTCAGCCAGAAGTTAGGACATTGTGATCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCTCTGCAGGCTCTGGTTGTC[CT]TCATTTGCAAAATAAAACCCA GACCGGGTCATCTTTCAGTCCCTTCCAGCTCTATTTTATGATTGCTCTTAGTCTTTATGAGCCA TGATGATTATCAGTCTCCCTGATGCACTCACTCCAATGATGCAAAAG
WI-22290a	136 C T ---				GACGTACTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGGTTTATGGGCCTCTAAGCACCG GCCAGTAGTGGGAATGCCACATGCATGGGTGAGTGGGATCTGGGGGGGTGACGACCTTGCTTTT [C]/TTTCCAATCTCTCTTCTTAGCCAGAACTTTGCGAGAGCCCTTTNATTTCTCTTCCCTCTATTCC CCTCCTTTCCCAATGTGCTAAGGTCCCAATTCAGAGCCCTCCAG
WI-22292	53 A G ---				CCAGTGAAGGGTTACAGCCATAGTGAGGTTCCCCCATTTGCTCAGTACCAGA[AG]TTTGAGTAC GGTGGTTAAAAATACTTATCTGACCACAGTGGAAA
WI-22387	186 C T ---				ACCTTGACACACTGCCATCCGGTGCCATCTCCTGGTGGCACATCTATCCCACTCTGGCTCTGAAAG GCTTGCAACCAAAATGGGAGCTGGGCTAAGGCATATTTAAACAAAGGCTCCAAAGACCCCTT TCACTTGGGTCTAGCATCCAGCTCTCTCAGCAAAAGGAGGATTGTTGTC[CT]CCTTGTGTTTCTG AACAGGGCCCAAGGGCAGCCAGGCATGCCATCACTGCAGCACTCAACCCCT
WI-22395b	127 A G ---				GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTTCTTCTTGAATATTTT GTAGGGATGGATGAATTGAAAGTGAATTAAAGTCAAGATAAAGGGGCACTCTTTAAT[AG]AAG GAAATGTTACCAATCCATAGTGAAGAGTGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCCAGG CTCCT
WI-22405	90 A C ---				TTTATGGCTCCTGAGTGCCCTCACCCAGCTACACTTTACCTTGTATCTATAAAGTGTAAATTTAGAGT AAATACATTTGGCTGTAAGTCG[AG]GATCAGGTGCTCTCCACCAAAAGCAAACTGCTGA AATGTGGCAAGGTTTCTCAGTG
WI-22419b	67 T C ---				CCCTTCTGGACAGTTTGTCTTATGTGTTTCAGACAATCAAGGTCGCCCTTCCAGGCACAGCCAGTGCIT [C]CTGGATGGCATCAGCACAGGCTCCCTGCCCGGCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59 T C ---				ATTTTCCCTTCTGTGTTTGTATTTCCCTTTTGTGAGTAAATNAGCAATACACTGA[TT]CTGGAA ATCTGCATGATTAAATAACATTAAAGTTCATAACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCCTAACCGAATGCAAAATAGGTATCCCTCAAAATTGACATTTCTCCTCTAGTT T

WI-21763b	154	A G ---	---	CATACCCCTTTAGTGCCACATTGATCTTGTAAACAGTCTTGTAGTTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACCTTCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATTG G CAGACATTGCCTGTGCTTCCCTACCCACAGCAGCTGTCTAGTGCACTT GA
WI-21763a	135	T C ---	---	CATACCCCTTTAGTGCCACATTGATCTTGTAAACAGTCTTGTAGTTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACCTTCCAAGTGGAGCCAGGCCTCAGACTGTTCTCAGTCACT T C GCTCTCCACAGCTGATTACAGACATTGCTGTGCTTCCCTACCCACAGCAGCTGTCTAGTGCACTT GA
WI-22440	64	A C ---	---	CAGTCCATTTGAGTCCCCAGTCGAGGGTGCACTTCTTCTTATCTTGTGTTAAGCCACTTGGGT A C TCCATTCAGCTCTGCACCTTCTCCAGTTTTCATGTCAAGAGTCCCTGGAGGGAGGAGGCTTTCTGG AAAT
WI-22449	74	T C ---	---	CAATGAATGTTGTGGCATATGATTTNCCATTGTGTGACAAATTTATTAGCTGGCATCCGAATACAGTAC TTCTTTT C GAAAAAATACACAATGGGAACGTACA
WI-21965a	112	A G ---	---	CAGGTTCCACCAGAGGCTTTATTTACGCCACTCAGGACCCCTGGCTTCTGCTCCAGGCACCTGAACA CAGTCAGGCTCTTCTAAACACTGGCAGGACCTCCCCACAGC A G CCCCACAGGGTCTCTGTT TCCCAAGTCCCTGATGGATTAGGCAAGACCTTACACATTCACCACTACCTGCTGGAGAGGAGGTC ATGAGGCAGCCTGTGGTGCCAGCTCAGTGTACACACTGCCAATGTGC
WI-21687c	115	C G ---	---	CACCTGGCAGTTGATCAGATTGTAGGAAATTAACCCAGATGGGTACATTTTTNTTCAAGTTCA AACCACATGGTTCCCTAGTCAGAAAGTCTCATGGACTTCTTCTTAAG C G TGTTCTATGATCAGAC CACCTCCTAAATGTGGCTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGACGCTGCTGGAG AG
WI-22374a	149	T C ---	---	AGCTTTACAACAAAGCGAGGTTTAAGGAGCCTGAGAAGAAATTCACAACCTATTGACTATACAGAG TCTTCAATCCAAAACAGTTAATAGTAACCTGGTGGCACATACAATGCATGCAATCTCTGTAT TATTAGTAACATAAT C AGGNTCCTGCATCATTCTCTTCA
WI-22250b	132	C T ---	---	ACTTGTCTTCAGGCAGGCATTTCTGGGATCTAACTAGAAATCCTTGAAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCAC T G ATG GGGTATTATG GGGTCTCTGCCTCCTGGCTGTGTTATG C T GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
WI-22250a	89	G A ---	---	ACTTGTCTTCAGGCAGGCATTTCTGGGATCTAACTAGAAATCCTTGAAAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCAC T G ATG GGGTATTATG GGGTCTCTGCCTCCTGGCTGTGTTATG C GGANCCAGGAGTGGAGGAGAGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192	G C ---	---	GCAGCCATCCTCTCTCCAACACTCCAGGCCACCTGGGGCCAGAGCACCTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCCGCTGGCCCGAGTTCTCGGCTCTCAGGACGTCCAGCAAGTGGA GCCAGAGGTTTGTCTGGGACTCCAGCCAGGGATGAGGCCACAGCCCGAGCAACCTG G C AGTGTCTC TTTACGGGGCGCGGTGCTCAGCTCTCTCTGGAGGTGAGGAAGGAGGT

UTR-04932-2a	149 C T ---	---	GCAGCATCTCTCTCCAAACACTCCAGGCCACCCCTGGGGCCAGAGCACCTCATGTGCCAGCAGCACCTACGTGGCCGAGTACGACCCGCTGGCCCCAGGTTCTCGCTCTCAGGACGTCCAGCAAGTGAAGCCAGAGGTTTCTCTGGGACTCCAGCCAGGGGATGAGGCCAGCCAGCCAGAACCTGGAGTGCTCTTTGACGGGCGCGCTCTCAGCTGCTCTCTGGAGGTGAGGAAGGAGGT
siFIBBb	412 G C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAAGTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCACGGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCTGGCCCTCTCTGATCATGCCAGGTTTGCAACAGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCCTCTCTGAAGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siFIBBa	341 T C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAAGTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCACGGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCTGGCCCTCTCTGATCATGCCAGGTTTGCAACAGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCCTCTCTGAAGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siGLV2	61 T C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAAGTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCACGGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCTGGCCCTCTCTGATCATGCCAGGTTTGCAACAGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCCTCTCTGAAGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG10017c	70 T C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAAGTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCACGGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCTGGCCCTCTCTGATCATGCCAGGTTTGCAACAGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCCTCTCTGAAGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG10017a	33 G A ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAAGTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCACGGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCTGGCCCTCTCTGATCATGCCAGGTTTGCAACAGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCCTCTCTGAAGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG10023	63 A T ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAAGTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCACGGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCTGGCCCTCTCTGATCATGCCAGGTTTGCAACAGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCCTCTCTGAAGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG10096	36 G C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAAGTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCACGGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCTGGCCCTCTCTGATCATGCCAGGTTTGCAACAGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCCTCTCTGAAGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG10118	107 C A ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAAGTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCACGGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCTGGCCCTCTCTGATCATGCCAGGTTTGCAACAGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCCTCTCTGAAGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG10120	89 T C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAAGTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCACGGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCTGGCCCTCTCTGATCATGCCAGGTTTGCAACAGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCCTCTCTGAAGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
siSG10178	42 C T ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAAGTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCACGGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCTGGCCCTCTCTGATCATGCCAGGTTTGCAACAGCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCCTCTCTGAAGGACCAGTCTGGTTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT

[illegible]

EST22917 6	74 C T ---	---	---	GTAAACCTTGC AAACGCCATGCTAAATGGAAGCCTGACTGACCAAGGGCTCTGGGCTCTCAATGCA ATAGAAAC[CT]TGACATGGGGCCAAAGACTTCCAGACAAAGCACGCGAAGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---	---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGAACCTTAACCCCTCAGGCTGTCTACTCA[GT]GTGGTTTGTAGCCTCACTCGACACAGGAAGCTTGAATTTGGAGGCTCCAAGTCACTCTCCA GAGGGGAACTTCAAAGAGGATTCCAACAGTGAAGCAGATCATGGGGCAAAAGTC[AG]CTATGG GGCAGACTGAGGTGGACCACACAGCACTCCAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCAGGAGTAGCCAT
EST36745 3	56 A G ---	---	---	TGTGACCATACCAACCTATGCAATAAAAGAAAAGAAAAATCCTCACCTTAAAAAAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTGG ATTTATGGTTTGAATAAAATACAAAATGTGTATCTCCTGAGACACATTTATAACATTTCTGGTATG T[AT]TATTGTGAGTGGTGTCTCTAGTGGCCAAT
STS- R37410c	201 A T ---	---	---	TGTGACCATACCAACCTATGCAATAAAAGAAAAGAAAAATCCTCACCTTAAAAAAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTTGG ATTTATGGTTTGAATAAAATACAAAATGTGTATCTCCTGAGACACATTTATAACATTTCTGGT ATGTATATTGTGAGTGGTGTCTCTAGTGGCCAAT
STS- R37410b	139 G T ---	---	---	TGTGACCATACCAACCTATGCAATAAAAGAAAAGAAAAATCCTCACCTTAAAAAAACAAAA AAAACCTTTGCAATGCTATCATTTTTCAGGCTTTTGAAGTGTGAATAAAAGTTCATAGCATTTT GGAATTTATGGTTTGAATAAAATACAAAATGTGTATCTCCTGAGACACATTTATAACATTTCTGGT ATGTATATTGTGAGTGGTGTCTCTAGTGGCCAAT
STS- R37410a	48 C T ---	---	---	TATCGTGGGAAGTTCCAACTCATACTTATGCTGCTTTTCTACTTGCTAATTTGGATGCTTCTTGCCA GGCTC[CT]TAAATTGTGCTGTAACTGGGAAGAAACCTTCTACTCTCCACAAACCTGAA
STS- R42778	74 C T ---	---	---	CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCTCCCGGGATGGTGAAATGTTCCGGACCTAGATA[CT]GTGACGA AGGTAGCAGCAGTGTGAGTGCACTAA
UTR- 04350	125 C G ---	---	---	GAAATAAACTAAAACTGCAAGCAATCACTGTAAATAAGAAATTGTTCTTCTGTTT[CT]GACAGTTG AAGTGGGTGTGAGATGGCATAGCAATGAACAGTGGGAGCCCAATGAGGTCTCAGAAATGCGGGCAAA CTCCTCTGTGAAAATGTAT
stSG1026 6	55 T C ---	---	---	GTATAATTCAGCATAGCCAAAGCCTTTTAAATAAACCAATACATATTTTATGAAATCTTTTACA AGAT[GT]AAGCACAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
stSG1028 2	70 T G ---	---	---	CACCTTAGATAGGAAAATGGTTTAAATGGACACAAAGGAGTCAGCCACGTTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTGTATATGCAATAACAGCAAAATAATTTTTCACCT[CT]ATG TCAATGCCAATGCATTGAAAGGCCCCAGAAAATGAGAAAAGGATAACAACTTTTGTATAAAAAGGTA AGAATTTCTGTGTG
stSG1031 0	128 C A ---	---	---	

stSG1033 1b	116 T C ---			TTTAAAGCTACATGTCTGAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTCGG GCTCCAAACCTGTCTAGGAAGGCTAGACCTCAACACCAACACCTCCATTC/GCATTTCCTCTTGG CTACTATGTCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1033 1a	107 A T ---			TTTAAAGCTACATGTCTGAAGAATGATGCTGCTGATTGAAATAAAGGAAGAAAGGATGCATTCGG GCTCCAAACCTGTCTAGGAAGGCTAGACCTCAACACCAATTCACCTCCATGCATTCCTCTTGG CTACTATGTCTTTTCCCTGACTTCTGCCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCTCC
stSG1243 b	225 G A ---			ATTGGCAAAATGGGAAAATGACACCAATCATTTGATTACAGAAAAATGGTTTTATAATCCTCCTCTTG AAATTATGTTTCAGGCCAGCATGGTAGCTTATGCCTGCAATCCAGCACTTCGGGAGGCCAAGGAGA AGGATCGCTTGAGCCCGAGAGTTCGACACAGCCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTTAAAAAAGAAATTCGTTCG/A/AAAGTATTTCAAGACCAAAAGGAGGT AACTGACGTATCACAGGGGCAAGTATCTCTGCATAAATTTGAACCTAGTTTGTCTTCTTAC/G/ACGCT TCACATTTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA AACTGACGTATCACAGGGGCAAGTATCTCTGCATAAATTTGAACCTAGTTTGTCTTAC/G/ACGCT TCACATTTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA TTAATGTCATCCAGGAGGGGCCAGGATGAGGGGAGGGTTGAGGAGCGGAGGCGAGTTATTTT TGGGTGGGATTCACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTGTT/GJTCAATCATTAAGAA GACAAAGGGTTTGTGAACCTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTCGTGG
stSG1385 b	117 T G ---			TCGTCTCCTTTCCAGTCTTCTGCCAGAAGCATCCCCATGATGTTGTGACCGCACAGCACTTTGTGTCT TT/C/GCTTTGAGCACTTGCCACTCTGGCTGGTCTGCTGCCACTGATTGTGTACTGCTTGTGCTGCC GATCTGGTTCAGACAAGGCTGATTCAGAGACTCCAGTGGTCAAGGCTCTGTTTGTCAATCCCT TGGTCCCTCCACTCCAGTTTGGCTTCTGTCTCA/T/CJAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTCACTGCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGTCCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
stSG1427	103 T C ---			CCCTGGAGTTTCTGAACATAGGAAGAAATGCAAGTCATGTGTTAGTCCJ/GJCTCCCTTGCATGA AATGTGGGAGAGGGAATAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1471	50 A G ---			CAAAACCAAAATCCTTCCACGATATATACTATTAGTCTAAGT/CJTTTAAATCAAGGTTGAGA ATGACGAATTCAGAATTTCTTTACATACATAAATTCCTTAGTTCTGCAGATGGGTA
stSG1483	44 T C ---			CACACCCACAAGTTTCATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCCAAAACCCAGTGTGCA J/CJJAATGTGGAGGATGTCTGTTGCAGCTGTAGTTACTAATGCAGGAAAAACCCCAATGCAAGAGGAA AATGCTCTGA
stSG1696	67 C G ---			

stSG1847 b	95 G A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAAGAAATTT AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTTCCAAATGTGAAACCAAAATTAATAAATACTTGATCACTGTGCT TCAACACAACTG
stSG1847 a	49 C A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTAC[C/A]CTAAATGAAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCGTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTTCCAAATGTGAAACCAAAATTAATAAATACTTGATCACTGTGC TTCAACACAACTG
stSG1897 a	83 A G ---	---	CTTAATGCCCTTCTCTCTTGCACAGGAGACACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGACACAGGACTA/GGCCCAACCACTTCTCTCCCGTCTCCCAAGATGACT
stSG2022 a	86 T C ---	---	TGCTTGAGGTTTCAAACTGAGATATCTATGGCAAGTTTATAAAAGTACATTGATCAAGGTACAA TTTTAACATTAAATATACAT/CJATTCATAATCTCATCTATTTAACATTAAACACAGGCCTTTGTGT TGTTATTTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGCCTCAGTTGGGGGTTGAC T
stSG2076 a	104 C G ---	---	AAACGTTGTCCCAAAATTTGTGTTTCAGTTTCAAGTATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAACACACTTAAGAATATATTTTGACATT[C/G]ACATCAGTGGGGCATTTT
stSG2108 c	71 A G ---	---	TTGAGCAACAATGATTGCGAATTTGGCAGCTCCAAACCAAAATGATTGAGGGCTCCACAGAGA GAGC[G/J]TAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGCTTTGATTG GTTACAGTTACACAGTTGCTTATTGGTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 T C ---	---	TTGAGCAACAATGATTGCGAATTTGGCAGCTCCAAACCAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAAGCAAGCAGCTTTGATTG GTTACAGTTACACAGTTGCTTATTGGTCTATCTTATGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2141 b	173 A G ---	---	TTATCCAGGGGACAAAGCTGCACAAAGGAATGTTCTTCTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGGAATAATCTCAGAAATGGCAGCACCCTGCGATGGCGATGGTGAGGTGGGT GCAGTCCCTGTGGTCTTATGCTTGAAGAGAGAAAG[G/A]GTAAGTTCCCTATTATTATTTAAGGC AGTTTCAGAGCACTGGCATTCTGTTGCTCTG
stSG2141 a	113 C T ---	---	TTATCCAGGGGACAAAGCTGCACAAAGGAATGTTCTTCTATTTTAAACAAATGACTGCGGTGAC TGAATCTGACTGTGGAATAATCTCAGAAATGGCAGCACCCTGCG[C/T]ATGGCGATGGTGCAAGTG GGTGAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGTCCCTATTATTATTAAAGGC AGTTTCAGAGCACTGGCATTCTGTTGCTCTG

stSG2148	50	A G ---	---	TGGAAACAACCGGCTATAGTCTGAGTCATATTTTATAGACCGTGATTTTC[A/G]AAAGAAACAATAA ATGTGGATTAGAAAGGAAACATCCATTACTGTATTTTCGATACTTGTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68	C T ---	---	CTCAATGAGGACTCCATCAGCCAAAGCGGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGCT [C/T]GCCGGTGACTCAGCTAATGCTACCGGGTTGGAGCGCACACCGAGCCAGCCACCTTTTCCAT AAGTGGCAGAGGGAAGGAGTGAAGGACCA
stSG2189	41	C T ---	---	CAAGTGGTGAAGCTGGGATTGAGCCTGATATTCACACTA[C/T]CTACATTCCTCCAGTATAATA GGAACTCATCGCTAACTTTTGAGCACTTAGTGTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTCGAAC
stSG2200	49	T C ---	---	TGTTGATGACCATAGAGGATGCAAGCTCCGGGCTGGTCTGTATGATG[T/C]TTTATATTTATGTAT AATGTCTTACCTGATGATACCCAAACATATTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85	G T ---	---	CATTTCTGCCTCCTGCTTCCCAGTACTACCCCGTCCAGCAACTGCCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAAAG[G/T]AGAGCATCTCCTCAGCCCTGGAGACAGTGTGGAGCTTCAGCT
stSG2257	65	A C ---	---	TCAGTATTGTAGGAGCTGGTAAGTCATGTCCTAACTCTGTGAGGCAAGGCTATCAGAAGGGCAG[A/ C]GTGCAGGAACCTCGCCAAGCACTGGGCTGCTGCTCAGGCAGAAATTTCTCCT
stSG2306	67	A G ---	---	GTCATCAGCGTAGAGGTCACTGGTATAACAACAGTAGCTATATGATATTTGGGAACATTTTACA [A/G]TATGCTCCCATTTGGGTTTCCAACTGATACAACCATGAGGTGAACACTTTTCACTGTTTCACAG TTCTCCAGAGA
stSG2334	70	T G ---	---	GAAACTACCCACAGCATCATGTTAAAGAGAGAGATGAAAGAAAAATCCCCGCAAAAAACA AAAAAT[G/T]GCAGTGGAGGGGCTGTGGAGGGTGAATG
stSG2339	63	T C ---	---	AGAGCAGATGGTGAATCAACAAGACCTCAAATTTGCTTGACTGCAGAAGTAAGTGTGCTAC[T/C] GTTCTCAGAGTCACCATACGGTGACTGTGCTATTTCTGGCTGTGCTTCTTCTATTCATCA
stSG2465	76	C T ---	---	CAAGACTAAGAAGCCGACCCGAGTGGTCCCACTCAAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTTCAAAGTGTGGGTATGCA
stSG2549	140	T C ---	---	TTGCAGGCTTGATTCACAAATAACAAGTCATGTATAGAGAATGTGAAATGATGACTTGAAAAACCAA GATATATAAATATTGAAGTCATTTATGCCCTTTTGTGACTGGTTAAATATGCAAAGCAGCTAAAG GAATATT[C/T]ACACACCCACCCCTTTTAACT
stSG2577	123	T G ---	---	AATTGCCAATGGAAATTTCCAGAGGATTTTAGACCACACTTTGCCCTGTGCTTCCAGTTTGGT CCCAATATAGGCCCTCTGCAAGAAGAGATCAATGCCGAACCCGAACTGTGAAGCA[T/G]GAACAATC CCGGCCAGATTAAATTAT
b				

stSG2577	121	C T	---			AATTGCCAAATGGAAATTCAGAGGATTTTAGACCAACTTTGCCCTGTTCATCCCGTTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAG[C/T]ATGAACAATC CCGGCCAGATTAATTAT
a						
stSG2700	58	G A	---			ATCTCTCGACTGCTTTAGTGGGAAAGGAATCAATTTATGAAGTCTCGGGCCCC[C/A]AGTCAC TCAGGTTTGGGAAATAAACCACTGGTCCAGAGCAGAGGCTACTTTGAGCCGGACACCA
stSG2724	101	T G	---			AAACAAGCTTTGTCAATTTCCACTACATTTTGTGTCTTTATTAATATTTGCAATGCTATAAT TTAATACTTATATCCAAATGCTTGATAATCA[T/G]TTTTTTTAACTCTGGGGTGTGAAGAAC
b						
stSG2776	65	G A	---			GTGGCCGATCTTTACTTTCCAGAAAGGCGGTAAATAAAACCTGTAGAAAGTCTCGAATATGC[G/ A]ATTGGCCCTTTGGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCAACCAAAAA ATATCCACTAATCCCGAATATAGTAACCTGCTTTGTCGGAATG
a						
stSG2791	109	G T	---			AAGGAAAGGTGGAGGGAAGGGAAGAAATACAATGGTTAGAAAGAGCAACTAAAGATTATTC TATTACTTCTGAACGGTAACTAGCAATTTTAAATAATTT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
b						
stSG2791	100	A G	---			AAGGAAAGGTGGAGGGAAGGGAAGAAATACAATGGTTAGAAAGAGCAACTAAAGATTATTC TATTACTTCTGAACGGTAACTAGCAATTTTAAATAATTT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
a						
stSG2826	85	C T	---			CCGCAATTTCAACACACATCTATGAAACTAAGGGTGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAAACA[C/T]GAACAAAAATAAGAAAGAAAAACCATGAATGCCAGGTTTA ATTTTTTCC
stSG2850	88	G A	---			ATGGGTGCATTGAAAAGGCAATTAATACTTTTCAGGCAGGGGCTGGCAATTTAATGAGCTGA TGTGTCCTCAAGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCTCCCAT
stSG3031	71	T C	---			ATACTACGGGGCTGAAGGCAATGTGAAGAGTGACTGCAAGTCTCGCATTTTCTGTGGTGCAGC AAAT[C/G]CCCCTTATTTTAAATGATCCAGACATCTGGGCAGCATAGCT
stSG3058	81	G A	---			GTCCCAACTCTCTCTCTTTAGAGAAAAACTGTGATTACCTCAACTTGAATATGAACGTGTGATTG AAAAAAGTCAAAAC[G/A]TGAAGAAGCATCAAGCCAAAAAGGCAAACTGGCTGAGGC
stSG3092	94	T G	---			CAGCATCTCCAGAACATTCCTAGAACTGAACCATCTTGTCACATTGAAAAACAAGCCCAAGTTC CAATCCAAAAATAAATGAACGTGC[T/G]GATAAACATTCTTATGGTTCCAGCCCCCTACTTT AGTT
stSG3230	95	A G	---			AAGAACTACTTTGGTAGCTATTTAAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTTAGTCAATTGTGAGTGAGTC[A/G]GTGGGGTGTCTAAGTGTCTGAACCTGAAGTAG
stSG3245	160	G C	---			ACATCTCATACCCAGTAAGATCAAGAAAGGAATATCTGAGAGCAAGCCCTGCTCCAGGGGCC CAGGTATGTGTAGAGGCCAGTGGGGGTGGCCACTTGGTGTTCACACCCCCCTGCCATCCAGTCTG GCCCCAGTACCTACCTGGGAGGTT[G/C]GTACTTGGCTTAAGTACTCAIGCTTTAT

stSG3265	42	T C ---			AGGTAAATGAGTTACTAAATGTAGCATTATTTATAAGGAAT/C/GCATTGTGAATAGTTTCTCAG TTTTCAATTATGGAAAGATGATGATTTACGCCCAATTCAGTGATGTTCTAAATAACACAATCGAC AGGACTGTCTGTTGATGATGATGAGGACAGCTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGTCTTGTGAGCTGAATTTCTGGGCTTTATGTGGCAGTGTGGTAAAA
stSG3269 b	141	C T ---			TGTAATCTACTGTGTCATCTATCCATTCCTTCCCTGAGCCTGGACTGCTCTTCCAAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATAGCTCCATAGCCATGCTAAA GCATGA/C/TTGTAGATCCCAAAGTCCCTGACACATTTCTTCTAAGAAACT
stSG3269 a	24	A G ---			TGTAATCTACTGTGTCATCTATCCATTCCTTCCCTGAGCCTGGACTGCTCTTCCAAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCTTTAAGCTTGATAATAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAAGTCCCTGACACATTTCTTCTAAGAAACT
stSG3284	130	C T ---			TTAACCTCAAGAACTTTGAGTTACAGGAAGATTTATCTAATATAAATGACTAAATACAAAAAGC ATAAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA[C/T] TCCCTAACTTTGTAAATGCTGTAATGGGACATTTGTGTTTGTATCTACCC
stSG3292	99	A T ---			GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAAAATCGGTACATGAGGCTTAGACATA CACATCAATGGACAAGTGACTTAAATATCTAA[A/T]TACAAATCAAAATAGCATTTTCTTAACCTCAA TAAATGTCATATCTTTAGCTCTCACT[C/A]CCAGTGATCCATTTCCCCAGCCGTAGAGCTTTCTG TTCTGTAGATTTGCCTGTCCTGGACATTTGATAATAAGGAGTTGCTGTATCATGTTGAGCTTCTCTC ACCTAGCATGATGTTTCAAGACACATCCATGCTGTAGCATGCGTCAGTGCCTTTCATTCCTTTAA GATCCCCAGTATTTCTAAATGAACCTGTTGTGGAAATAAATACTGAGGACCCTCAGAG GG[C/T]TAAAGGGAACCTCTTTGCTTAGTTCATAAGGACTTTCT
stSG3369	69	C T ---			CAAGACTGTAAGAACGTAGGCCCTGTGAGAGTGAAGGAAGGATGCTCGAACCTGCCAGGACTCAGG CTTCAGCTTCACAATCCGAGGAAGGAATGACATTTCCAAACTGTCACCTTTGTAGC[G/T]CTGGGT CAAAGTCTAAAGAGGACAAATAAATAGAGACT
stSG3398	125	G T ---			TCCTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG[A/G]CTCACTGTAGCCTGGACTCC TGGGTTCAAGTGATCCTCCACCTCAGCCAACTGAGTAGCTGGCCTGCAGGACAAGTCACCATGCCTA CCTAAGTTTGTAGAGACAG
stSG3416 a	43	A G ---			GTAAGACAAGGTTTGTCTATGTTGACCAGGCTGGTCTTGAACCTCTGGCTCAAGCGACCGTACCA CCTTGGCCTCCCAAGTTGCTGATATTACAGGTGTGAGCCACTGCCCCCGCCGACTTTTAACTGAAT GTTGAAAATCATCTGCTCTTTGCTGGGTAACACTGA[T/A]CAAGTTGCTTAACCTTTGTGAAACCCAC TTTCCCTATCTGTAACAAAATGGACAACAGAACTTTTCCCTTCCCTCTC
stSG3424	173	T A ---			GTTTCATGTTAAAGATTAGGAAAGCTGTGGATGTGAGGGGTGAGGTGATGTGAGGCGCTCACAGA ATGAGTGGCAGAGAGGGCCCTT[A/G]AAATAGCTTACTCTGTTTCTCTATC
stSG3436	88	T A ---			

stSG3463	103 C T ---	---	---	GATACAGAAGATAGTGTGGTATGGATAGTATGAAGGACAAATAATACAAATATTTTATG AAATAACAAATAATGCATACAGCTCAATGGGTAC[C]/TGGAAACAAACTTGGCTTACTATATTA CTGA
stSG3491 b	71 G A ---	---	---	CAAGTACTTCTAATGCTCTAAGTAGTGCAGTCTGGCAATATTTCTCACGAACAAGGACGATTG AAGA[G/A]GTGGAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCCTGCAATTTAGCAGTCTGA ACAATCTTCTAATCTTTTACTGGCACCTGTGGATTCTATTAACTCATTTACTATTTTCTGTGATG ACAGAAATAAGTTAAC
stSG3523	33 C T ---	---	---	TAGCCATCTTACTCTAGTCTTTTGGGTTT[A/C]/TGCATATATGTGTGTACAAACACACACACC CCTAATTCCTCAATGCTCTTGGCATAAGTTTATCTCTACTGGTCTC
stSG3536	213 A G ---	---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGTACAAACCAAAATACAGAATGGCTTC TGTGATACTGGCCTTGGTGAACGCACTCAGTCTCATTTCTATTGTTTAAATGAGCTTG TGCACCATTA[G/A]GTCCCTGCTGGGTGTTCTCAGTCTTGGCCATGAAGTATG
stSG3583	112 G A ---	---	---	GAAAAAGCTTAACATACGATCCATGTGCAACCCCAACAGGATCTACGAACTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAAGTGCACATCCACACAGGCAC[G/A]/TAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586 a	60 G C ---	---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAAATCAGGTGTGGTGT[G/C]/ACG CCGTAGTCCCTACTTGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAAA
stSG3589	101 T C ---	---	---	ATATAGTGTGGTAGCATTATAAATCCTTTAAAAAGCAATCTGGCCATATCAAAAGGCAAAAAAGT GTATATACCACCTGGCACAAAAACCCCAATGAT[C]/CCTATTTCCAAAGATGTATCCAGATGAAA GTATCCAAACAAAGCTATATACAC
stSG3590 a	70 A T ---	---	---	GAGAGATGAGCTATTTTACTTTTACTTAATGAAGATGTAAGAAATGATCTTCTGTTCTAAAAAAA AAA[A/T]TTTCTCTGATGCTCTTGACCTGTAGGAAACACATTCAGTTTCTACACT
stSG3619	78 A C ---	---	---	CAGTGAGACTTCTCATTTTATAGCAATACATTTTTCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCTTT[A/C]AACAAACTTCCAGAGAAAACTGGGCTCTATATATTTAAG
stSG3644	40 T C ---	---	---	ACATATGTAACCTGCCATTAGTAGCCATATTTAGGATGAGA[T/C]/GGATTGAGAGGCGCATGAACCAAGG ATGCGTAATAATCATTAATGAATAAAGTTATCTGGGGAACCGGCCATTTGTCCCAACATTTACTAA GTGCTACTA
stSG3646 c	70 G A ---	---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGATATATGATGATAACAATAATATGCTTACT GGT[G/A]ATTAACCTTGTGATCTTGGTTAAGATGGTGTCTGCTAATTTTCTCCATTGTAGAGTCATT CTTCCTTTGTA

stSG3646 b	55	A G ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAA/GJTATGTCTT ACTGGTGATATTAACITTTGATACITTTGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43	A T ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG/JTJGATAACAATAATATGTCTT ACTGGTGATATTAACITTTGATACITTTGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85	A C ---	---	ATTGTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCCGATGACCATCCAACCCCTGGACTCACCT GAAATATCCTACGAGGC/A/CJTCCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3693 a	30	C T ---	---	ATTGTTCCCTGAACATTCCCGTGGTCTCC/CJTCTGAAAGCCGATGACCATCCAACCCCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAAGG
stSG3698 b	145	G A ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGACCCCAATCCCCAGGGTTGCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAAGTCT TTATTGGG/G/A/JAGAAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51	C G ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGACCCCAATCCCCAGGGTTG/C/JTCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGAAATACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107	C T ---	---	ACCAGCCTGATGTCAGAGGGTCTCCTGCTGGATCCCCAACTGGAGCCATCCCTGGGCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGATGTGAAG/C/JACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGTCT
stSG3725	104	G A ---	---	GCCAAACAAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAAATATATTATTACAGCCAAACAGCAACAGCC/C/JAGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAATAACGGCACATTTA
stSG3751	128	G A ---	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTCATACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGGATATGGTCCC/G/A/JTT GCTGACTCCATGTGTGCAAGAG
stSG3787	49	T A ---	---	TTCTGTGCAAAAGAAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTAT/A/JAAAGTCCCTAAGA CACTGAGGGCATAAACCAACAAATAAATAAGGAGTATAGGCTAAAGCAGTATCTTCCCT
stSG3880 b	115	G C ---	---	GACAAGAGGGAAGAGATGCGCCAGAGACAGGGCTGGGCGAGCTGGGGTCCCTGAGTCCAGGGCG CACCACAGTCTGTGGGTCAAGGCCCTCCTCTGGGGAGCAGGTCTA/G/C/JGACACGGAGATGCAG GGCTGGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGCGCT

stSG3880 a	36	G C ---	---	GACAAGAGGGAAGAGATGCGCCAGAGACGAGGGGCTG[C]GCGACGCTGGGGTCCCTGAGTGCCAGG CGCCACACACAGTCTGTGGGTCAAGGCCCTCCTCTGGGAGCAGGTCTAGGGACGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGGACCCAAAGAGAGTCCATTTCTGCCCT
stSG3895	44	A G ---	---	AATAGCCATTGTACACATTGCAGCTATGATTTAGTGTGTA/GJT/TTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATTGGGAACAAGATGCTGATTCGTCAACTG AAAAT
stSG3902	104	T C ---	---	TCTGTTGAGACTGGAGAGACCAGGTACCAAGCACCAGCTCTGGTGGAACTGGCTTCCTGATAACA TCATCTATTTACCTAAATGTGAACCTGCTTTCTTTTC[C]TCAGCTCAATAGCTTAACATCTAATTC ATGTTGCTCCCTTTGCTGGACAAT
stSG3935	50	G A ---	---	GGGTGCTGACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTC[C]G/AJCTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGGTCAACAACCTTCCTGGACGT
stSG40	25	A G ---	---	GAGGAAGAGGTTGAAGAAGTCTGA/JG/AAATATATTTAAGATTTCTTGGGAGAAATCTCGTGC CCAAACCTGGTATGGATCCCTTACTATTTAGAAATAGGAACAATAAACCCCTTGTGTATGTATCA CCCA
stSG4009	32	A G ---	---	GTGTGGGCTGTCTGATGATGAATGGCGCGCTC[A/G]TACTTTTACGGCTTACACTTTTATGCTCCT ATGAATTTCTGATGGCTTTAAGGGCTGAACCATATCTGAAGTTTTCACACACTGCTTACA
stSG4033	123	T C ---	---	AGAAGCCTTGGGGACAATGGCAGTGGCTTCTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGAACCTAATGTTTTCAAGCATAAAGGTACTTTT[C]JGTGAAC AGTGGGCAACAC
stSG4038 a	29	G A ---	---	GCTGAGAGCACGTGTACAGCCACGCTGTG[A]GCGAGGCCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTACGGCTCCCGGAGAGCACCTGAGGGTTCCATCACT
stSG406	53	T C ---	---	ACTGTGGTTCAACAGTATTGCGTTGTGACAGCTAGGAAAGCTAAACGAACAAAAT[C]JGGTTTTAGTT TTGCTGAAGACTGGCCTTATTAATGGACAGCTTTCTCTAACAGAGATTATTAACTTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55	G T ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTGATCTATTGTCTGTAGATGTATTAG[G/T]ATAAAAA GTTTGCTTCTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4095 a	27	A C ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTG[A/C]GATACTATTGTCTGTAGATGTATTAGGATAAAAA GTTTGCTTCTGTAATACTTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG CCTTTGGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4120	65	G A ---	---	TGCATGTTCCACATCTTTTATAACAGCAAAATGTATAATAAATTAACCTTACGTACTTATGGATAATCAC[G/ A]CTTTTCCCCTCAGAGAGGCCACAGTTTAAACACGTTCCAGCACACCATTAATCCACCGAGCT

stSG4128	54	A G ---			CITGGCAGATAAGGGACTCGTTGCAGATATGACTTTCCTTTGTGTACATTCTT/GTATATTATTT TACTTCTCTGAAATGCCACATAATTTGCAATAATGATTCACTCCTTAGCTCCAAAGCAAGTCC TTTATCAAAATGCAAAATGTTCCAGAGGG
stSG4209					CACGAAACAGATGCAAGCTACACAGTCTGTAGGACCGAGGCTCAAAACATCCACATGGCACAAGC AGGCCCGGCACTCCAGGCAACGAAGCCACCCGGAACCTTGACAGGCGGCACTCCCTC/GA/GC AGGGGACCAACGAGGCGACAGGTGCTTTGATGCTCCGGAAGAGCTGAGCTCCATTCCA
b	128	G A ---			CACGAAACAGATGCAAGCTACACAGTCTGTAGGACCGAGGCTCAAAACATCCACATGGCACAAG /A/CAGGCCCGGCACTCCAGGCAACGAAGCCACCCGGAACCTTGACAGGCGGCACTCCCTCGGC AGGGGACCAACGAGGCGACAGGTGCTTTGATGCTCCGGAAGAGCTGAGCTCCATTCCA
stSG4209					CACGAAACAGATGCAAGCTACACAGTCTGTAGGACCGAGGCTCAAAACATCCACATGGCACAAG /A/CAGGCCCGGCACTCCAGGCAACGAAGCCACCCGGAACCTTGACAGGCGGCACTCCCTCGGC AGGGGACCAACGAGGCGACAGGTGCTTTGATGCTCCGGAAGAGCTGAGCTCCATTCCA
a	65	G A ---			CATTACCCAGAACGCCATGGAGGACCAAGAGC/GA/CACAGGCCGGGACTCCCGGATGGCTGGGGG GCTATGCTCTGACAAGAGATGACGAGGCGGCGGGGCTGCCTCCTCCCCCAGGGGCAGACGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCCGGTCATG
stSG4254					TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGGTAGTGGCTCCACACATTTCCAT TTAAGCAAAATAAATTT/GAGCTTCTGAGTAGTTGTTCCAGTTTCAACCAACATTTTG
b	31	G A ---			CTCACAAGGCCCAACACAGAAAAGATACAAATACATTCACAGCTAATAATTTAGTTTATGACAC AGAGT/GTTTTCAACAAGTTTAAAGTGTACCTGAAGAGCATGTTAAAGATTAAAGTTATCATT GGAGAGCAGATTTCTGGCCTCGCCCTTGATGCTGTTGAGGGGTGTC
stSG4301					TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC/GA/TAAGTGGGAGATAAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4331					TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGATAACTGCACTTTTGC/A/CJCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
b	71	T G ---			TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGATAACTGCACTTTTGC/A/CJCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4340					TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGATAACTGCACTTTTGC/A/CJCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4361					TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGATAACTGCACTTTTGC/A/CJCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
b	109	A C ---			TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGATAACTGCACTTTTGC/A/CJCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4361					TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGATAACTGCACTTTTGC/A/CJCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
a	24	T C ---			TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGATAACTGCACTTTTGC/A/CJCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4376					TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGATAACTGCACTTTTGC/A/CJCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
b	73	A G ---			TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGATAACTGCACTTTTGC/A/CJCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4381					TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGATAACTGCACTTTTGC/A/CJCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
a	50	T C ---			TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGATAACTGCACTTTTGC/A/CJCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4410					TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGATAACTGCACTTTTGC/A/CJCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
b	79	A/G ---			TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTCTTGGAATTTCCATAAGGATAACTGCACTTTTGC/A/CJCTTCACAACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG

stSG443	65	C T	---			AGCAGATCAGTCAGCCCACTGCTCTCTCTCTTTAGGGAGAGGCTAGGCAGTGAACACATCA/C/
stSG4430						TGTATGCAATGAGAAATAACCAACTGGTAGGATGGGGAGGGGAGGAGGCAATAGGCAC
a	54	A G	---			AAATGGAATCTATCCTGGCTGCTCTCAGGTC
stSG4448	99	G A	---			ATGCACATTAAATGAATGGCTAACTACTGGAACTTTAGTAGTTCTATAAGGT/A/G/JATTAAACATA
						GGTAGGATCCAGTTCTATGACAGGCTGCTGAAGAACAGATATGAGGCATCAAGAGGGCCATTTT
stSG4449	92	T C	---			CCTCCCTCCCTCTCTTCCCTTCCAGTCTTTTCCATACTGTTCCCTCCCTCCCTCCCTCCCTCCCTCT
						CGCCTAGCCCTGCCCTCTGGGCTCACTGC/G/A/JTGGGTTAGGCCCTCCCAAAA
						ATTAGCCATTCTTGCACAAATTCCTTACTGTAACCTAAGAGTACTGTACTGATGATGTTTACAAT
						TAACCTTTGGACAACTTAAACTTA/T/C/JAGTGACATTGCTGTCTAATAATCAAATACCTTCATCATA
						GGCTGAACATAATTATTAAAGAGCAAAAGTTACCCCTCCC
stSG4467	42	C A	---			CAGACATGAGGGATGGCCCTGCTCTCTGGGACAGAGCCCTCA/C/JAGATGATGTCCATGTTTGTGT
						GAATGAAACTCAAAACACTCTTCAGTTTTAGAGTCAATTTCTGGTATCGAGCGACCACACCGAGGAG
						CACACCCTGCTTCCAAGGCTGCTGCTCTGACACAGT
stSG4475	21	A C	---			ACATGTCAATTCCTGACCAGG/A/C/JATTAAATAGTTTATTAGAAGAAATGAGTTGAAGTGAGCGA
						TTAAGAGACACAAACTGGACTTTTGTTTCTTTTACTGTAGCACCCAGGTTTCATG
stSG4477	32	A G	---			GTAACATTCTGGGGTGGGGTGAGACAAACA/A/G/JATGAACCAATAATAATTACAATTATACATT
						TCAAGGAGACTTTTAATCTAGTTAATGTGAACGACGACCATCAATGTTTGTGAGGAAAGGGGAGA
						TGAAGTCTGCTCTGGGCAACGTTTGGCCCTCATGCACTGACACTGGC
						TGAAGTCAAGAGTGGTGGGAGCTGACGAGGAGGAGGCTGGGGCCAGATGAGCCGCGGGGA
						CAGCAGGCTG/C/JGCCACGTCCTGGCGTTGGTAGAAGAGGACATAGGCTGCTTGGACTCGATCT
stSG4531	79	C T	---			GATTCTCATTTGACAGGGGAGACGCTGTTGTCATCAA
stSG4550	86	G A	---			TGCATTAAGGAATGATACGGCATATTTGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATT
b						AAAAGAGACAGTGGGCACC/G/A/JCAATTTGAGGGGAAGGGGGCAGGGTTTATAGAGAAC
stSG4550	85	C G	---			TGCATTAAGGAATGATACGGCATATTTGGGGGACAGAGAACAGGCTTGATGAGGACAGAGTCTATT
a						AAAAGAGACAGTGGGCAC/C/G/JCAATTTGAGGGGAAGGGGGCAGGGTTTATAGAGAAC
stSG4590	47	A G	---			AATCAGGCACAAAGCTCGGGAGAGAGCCCAACAAAGCTCTTCTGCAC/A/G/JATGGGAGGGAGACAC
						CATTGAAAAGGCATGTTCTCTTCTCATGCAAGCGAGGCTGGCTCCACAGGCATGGTCTCCTTG
						AATCTGTATCACCCAGCGCTGGT/C/JCAATGTACTAGTAGCTTCCACAGGGATTTTATACTATTCT
						CTATAAGGTTTATCATGAATAAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTCACATTTATCT
stSG4623	22	T C	---			TAATATTCCTGTTCAAGATGCTCTGGAG
						TAAAAAACAACCCCCCAAAAAACACCCAGAGTTTTTATGTTTTTATGTTTTTATGATTTTAAAG
						GTATTTCTTTCTAGCTTCTAAATTTTGTAGTCAT/A/C/JATCAGAAAGCTTCCCTACTCACAAGGTGA
stSG4843	102	A C	---			GAAAGGA

stSG4850 a	38 C T ---	---	---	GGAATCTAAACTGGGAATGGCCGAGGAGGAAAGGGGCTC/C/CTGTGACCTTTCGAGGCCACGTCAGGAG AGCCAGCGGTGCTGTGCGGAGGTTTCCAAAGTGCTCCGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGATTCTTGGGTCC
stSG4879	86 A G ---	---	---	AACTCTGAAGGGGTGACCTCAACCCAGCCCTTGTCTGTGAGGTCTGCTTTTGCAGAAATGCGCTG CCCTGGGACTGGAGCAG/A/G/CTTGGGTGAGCTCTAGGTGGAGGGTGGTGGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104 G A ---	---	---	ACTGGACTGGCTGCTGAGCCGGCTGAGCGGGCTGGGACTCGGGCTGACCACCTCGCTCTTCAG AGACTGCCCGCGGTGACCACGACTACGCTCTGCC/G/A/GTGGGAAAGCAGAGCAGGACC
stSG4896	112 C T ---	---	---	AAACAAATCAAAACCAATCCCGAGCTATGTACAGGGCCACTCCCTGCTCTGCCATAGAGA GGTTGGGGGCGAGCTGAGGAGTGGTGGGGCTGGGCACCTTTCT/C/TCAGCCACAGGCCCTGAGG AATTAATTGACTG
stSG4932	22 G A ---	---	---	ACAGTGCCGATGGTTACACAAATG/A/JTTGTAATGTATTAATCCACCTTACGAATGATTAATGA TAAATCTTATGTTTATTCATCACTACCAAAAGGCTGGGTGCAGGGGTGCTGGTTTCTGGTCTT
stSG4950	24 A G ---	---	---	TCATGACTCCCGAGGAAAGGTCTT/G/CTTAGCTTCTCTCCCTACTTTCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 G A ---	---	---	AGATACGGGCAAAACACTGGGATGGCTTCTCTGACAACTTAAGAGGTCTCCGAGTTATTTCTGGGT GGGAAACACTGACCCAGCCCTTATTCCTCAAGGACTTAGTCATTGGCAAGGAGGATTTCATGAGCC CC/G/A/GTGAACACAGATGGGGCCCTGCTCTATATTCAC
stSG4961	91 C T ---	---	---	GAAGGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAGGAAAGTA/C/TJAGAGAGGGCATTCAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 A G ---	---	---	ACTGGTCCCTCTCAGCAGATTCAGGGGTGTCAGGGCTGGTTACCAAACTCAGTAGGAGTGCAA GGGTJ/A/GJTACCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTTCTCCCCTTTTCTTGTGTGC AACCTTG
stSG4997	22 T C ---	---	---	CAAAGGAGTAGGAGCCCAAT/C/JTTTAAATGGTTTCTCTCCCCTCATGCTATTTGATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTAGAAGGGAGGGAGGCAAGAA GGGATAGGGAGATGGTGATCCAAAT
stSG6312	37 C T ---	---	---	ACAGGTTCTCACACTTTGAGCCCTTAGTGCAAAACAC/C/JTATGCCATGCGGGAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATACCTCAAGCAGAAGAC
stSG6345 a	107 G A ---	---	---	GCTCTGGTCAAGCAAAATTCAGGACAGAGCAAGCAAGGACAGTAACACACATGTATGACCCCTTA CAAGTGTCTTAAAGATTTAAAAATGTGATGTTTGTCCAC/G/A/JATAGTTGAGGCAATTAAGAATAT GCAACCCAGAGAAATTTCTGTGAAACATTTTGTCTTTGGCCTGGTGTGGACAGAAAAGGGTGGCCAA ATGGATTGAGTGATGAGCAGCATG

stSG8145	97	CT	---	TTGTGGACTTCAAATCTCTTCCCTCAGATTTTAAATGACATTATGCATGTACATATTTTAAAAATTT AGACACATTTTAGAGAACACAATTGTGAA[C/T]ACAAATCTAAGAAATGAATGAGATGTTCTGAAAA TCTGATTCAAACACTTATCTTAAACTGACTTCTGTCAATCCTCTGCTGTGAAGG
stSG8150	36	AG	---	ATTGTTCTTGCAATTGCTTGGATTTTTCAGAATAGT[G/G]ATAAAATAATAACGGGAATCCTAGGCAT TCGTGTTTTTCTATGTTTTTAACAGGATTTTCTCTAAATGTTTCGCTATTAAATACCATGCAGGAAATT GGGAAAT
stSG8340	30	CT	---	AGAGGATTATGGAGAGAGCTGGGCAGGATC[T]CAACATTATGACCCCTGAACCTCCAGAACTGGAT TCACTAGAAGGAGAGAGAAAAACGCTCATCAAAA
stSG8466	111	GA	---	TGTGTATTGGGTGACTGTAGCCTAAGGATAAAATGAATAAATGACAGCAATGTTTATAAGCAGTGGGA GGAGTGAACCTGGGAATACTTGGTTACAAGGTATTGCACTACCT[G/A]TGAAGCAGCACAGCAATTAT TTGAAAG
ESTD-ACE	--	--	---	GATCAAGCAGTGCACACGGGTACGATGGACCAGCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTCCCGTCTCCCTGGTCGGGGGCCAACCCCGGCTTCCATGA GGCCATTGGGACGTGCTGGCGCTCTCGGTCTCCACTCTGAACATCTGCACAAAATCGGCCTGC
ESTD-ADA	--	--	---	ACCATCTTATACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCAGCTCCACCCAGAGGCCCTGGGGAATCCAGGTCAGTGTTCCTCTCCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAACTGGGACTGTGAGGAGACTCGGCCTCGGCACTGAGCTGCAGACCC GCAGACCAACTCCTGAGCTTCTGGGCCCTCTGAGTCTTGCTCTC
ESTD-AK-168	--	--	---	GGGAGTGACAGCTAGAGCACCAAGGGGGGCTCTACAGCTGTGTTCTCATGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	--	--	---	AATCCCAGCACCITTAGGAGGCTGAGGCAGGCATATCACCAGAGGTGAGGAGTTTGAGACCAGTCTGA CCAAATGGTGAAACCCCATCTCTACTAAATAACAAAATTAGCAGGGATGGTGTGCATGCCTGT AATCCCAGGAGGCTGAGGCAGGAGAACTGCTTGAACCTGGGAGCGAAGTTGTGGTGAGCCGAGAT GGCACCAATTGCACCTCCAGCCCTGGGCAACAAGAGTAAACTCTGCTCTC
ESTD-ANT1	--	--	---	TCCTCTGTCAATTCCTACTCCATTAGTTCAAGGTGAGTGAAGAACTGGGGCAATTAAACCAAGTAATTCA TGGACTGCCCAACTCGGAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD-APOA2	--	--	---	CCAGGTGTTGTGGCACGTGCCGTGTAATCCAGCTACTCGGGAGACTGAGGCATGAGAACTCTTTGAAC CGGGAGGCGGAGGTTGCAGTGAGCTGACATCGCGCCACTGCACCTCAGCTGACAGAGCAAG ACTCC
ESTD-ARSR	--	--	---	GGAAGAAATGGAGCCTGTGGGAAGGAGCGTCCGAGGGGTGGGCTTTGTGGCAAGCCCTTCTGCTGA AGCAGAAGGGGTGAAGAACCGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGACGTGTGGAAAACCATCAGTGAA GGAAGCCCATCCCCCAGAATTGAGCTGCTGCATAATATTGACCCCAAC

ESTD- AT3a	--	--	--	---	---	AGACCTCAGTTTCTCTCTGTAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGCCAGCACTG GTGCCCTGTGAGTCTGATCAGGTAGAGGAGATGGGACAGGTGGAGGAAATTTGAAAGGGCATTTG GAATTCAGAGCAAGAGACAGATATTAGAGCTGGGAAATGTGG
ESTD- B3AR	--	--	--	---	---	GGCTGCCAGGGTTCCGTGGAGGGGCGCTAGCCGGGGCCCTGCTGGCGCTGGCGGTCTGGCCAAC GTGGGAGCAACCTGCTGTGTCATCGTGGCCATCGCCGAGCTCCGAGACTCCAGACCATGACCAACGT GTTGCTGACTCGCTGGCGCAGCCGACCTGGTGATGGGACTCCTGGTGTGGCGCGGGCGCCACCTTT GGCGC
ESTD- BA511	--	--	--	---	---	GGGCAACATAGTGAAACCCCATCTCTACAAAAATACAAAAATTAGCCAGGTGTGTAGCAAGTGC CTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAG TGAGCCAAGATGGTGCCACTGCA
ESTD- BCL2	--	--	--	---	---	AGCTGGATTAACTCCTCTCTTCTCTGGGGCCGCTGGGGTGGGAGCTGGGGCGAGAGGTGCCGTT GGCCCCGTTGCTTTCTCTGGGAAGGATGGCGACGCTGGGAGACAGGGTACGACAACCGGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTCGACAGAGGGGCTACGAGTGGGATGGGGGAGATGTGG GGCGCGCGCCCCGGGGGCGCCCCGACCGGGCATCTCTCTCCCA
ESTD-BCR	--	--	--	---	---	CAGTGGCTGAGTGGACGATGACATTGAAACCCATAGAGCCCCGGAGACTCATCTGCGCAAGA GACCAAGAGGTGAGCTTCTGTGTCCCGGAAAGGAGGAGGTGACAGCTAACTCTGCTTCAAA ATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCTGCCACA
ESTD- BRCA1a	--	--	--	---	---	AAGAGAGAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAACTGAAAGATCTGTAGAGAGTAGCAGTATTCACTGGTACCTGGTAC TGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACCTAGGGAAGGCAAAAAACAGAA CCAAATAAAT
ESTD- BRCA1b	--	--	--	---	---	ACTAAATGTAGAAAAATCTGCTAGAGGAAACTTTGAGGAACATTCATGTCACTGAAAGAGAA ATGGGAAATGAGAACATCCAAAGTACAGTGAGCACAATTAGCCGTAAATACATTAGAGAAAAATGTT TTTAAAGAGCCAGCTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD- BRCA1c	--	--	--	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTGTCTGAAATGACATTAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGA AATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	--	---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCTCCCTAATTTGCTCCGGGAAGCACATTCAICAA CCCAGTCAGTTTGGGGGACAGCCATGCACCTGAGCCCTCTGGTAGCCCTTCAACCATGCATTCCATCTAA GCTCTGCAAAAT
ESTD-C6	--	--	--	---	---	

ESTD-C7	--	--	--	--	---	---	---	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA
ESTD-CB22	--	--	--	--	---	---	---	GGCAAGTTTTTATTGATAGAGAGGAATCAATAATGGCAATGAGGAGACATCACTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGGCAACCCATAGGGCGGATACAAAAGAC AGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGTGACCCCAAGCAAGGAGGACCTAG TAACATAATTGCTTTCATTATGGTCTTTCCCGGCCTTCTCTCACACAC
ESTD-CB23	--	--	--	--	---	---	---	TAGAACCAATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCATTATGTCTTTCCCGCCTTCTCTCACACATACACAGAGCCCTACCAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTCCCTTCCAGAGGACCTGAAAAACGTTCCCAACCCGA GGTCGCTGTGTTGAGCCATCAGAAAGCAGAGATCTCCACACCCCAAAA
ESTD-CB24	--	--	--	--	---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCCCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTGCTGTGTTTGAAGCATCAGAACGAGATCTCCACACACCCAAAAG GCCACACTGTATGCTGCGCACAGGCTTACCCCGACACGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTGAGCAGACAGCCCGAGCCCTCAAGGAG
ESTD-CB25	--	--	--	--	---	---	---	GTTTCTTCAGACTGGCTTCACTCCGGTAAGTGAGTCTCTCTTTCTCTCTATCTTTGCGGTC TCTGCTCTGAAACAGGGCATGGAGATCCACGGACACAGGGCGTGAGGGAGGCCAGAGCCACCTG TGCACAGGTACCTACATGCTCTGTTCTGTCACAGAGTCTTACCAGCAAGGGTCTCTGTCTGCCAOC ATCCTCTATGAGATCTTGTAGGGAAGGCCACCTTGTATGCGGTG
ESTD-CB27	--	--	--	--	---	---	---	TTTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGCCTGGTTGCATTTCAAGAGTGTCTGTGGAGTTTGTCTCATCACTGACCTATCTCTGA TTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTTCTCTCCACCCCAATGCTGCT TTCCTCTGTTTCATCTCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD-COL2A1c	--	--	--	--	---	---	---	AGAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCCCTGTCACTTTCAGGGTGTTCAGGGTGGAAAAGGT GAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACATACTGCCTTTG GTCAGCCTATTGAGCTGTAATCACCATACCCGTACCT
ESTD-COL2A1d	--	--	--	--	---	---	---	TGAGAGAACACCTAGTCTCCATCTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGGACCTGGAACTGGACTTCTTCTACTGCAGCAGACAAGACTTACCC AAGAGAGATTAAATGGCAAGATATACAATAATTTTATTGACCAAACTATCATGGAACACAGC ATT
ESTD-CPT2	--	--	--	--	---	---	---	GCCGCAATGCCCGGAGTTTCTCCAATGTGTGGGAAGGCCCTTAGAAGACATGTTTGTATGCTTAGAA GGCAAAATCCATCAAAAGTTAACTTCTGGGAGATGAAAGCTACCATCACTTCTCATCATGAAAAAC TGGGAGGCCGGCATAGTGTCTCATGCTGTAATCCAGCATTTTGAGAGGCTGAGGCGGGTGGATCAC TTGAGGTGAGGAGTTTGAGACCAACCTGGCCAACT

ESTD- CTLA-4	--	--	--	---	---	---	ATGGCTTGCCTTGGATTTCAGGGGACAAAGGCTCAGCTGAACCTGGCTACCAAGGACCTGGCCCTGCAC TCTCCTGTTTTTCTCTTCTTCATCCCTGCTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGCATGCCAGCTTTGTGTGAGTATGCATCTCAGGCAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	---	CAGGCCAGCGTGGTGGAGGTGACCATCCCGCAGAGAACAGGTCAGCCACCACCTATGCACAGGT TCTCATATTGAAGCTGCTCTCAGGGTTCCCTTGGCCTGAGCAGGCCGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	---	AAAAAACATTTTAAACACCTTTTCAATCATATACACCATAAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTTTCCAAATTAAGTCAATCTAAATGTCAATACTGATTAAATGCAAGTTCAACAGACA ACTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATTTATGCCCATAT CTGCAATGTC
ESTD- D17S33	--	--	--	---	---	---	CATCCCAAGCCCATCTCTTAGCCACTGGCAATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGGAAAGGCTCCTCTGGGGCGGTG GGGTTGTGGCTATGTGGTGGTCTTGTGTAGACGGGGCTTGGTTTCAGTTGCACCTATTGCGTTATT GCAGATTGCTTTGCTTTCCACTGAGCGAGCCTC
ESTD- D18S8	--	--	--	---	---	---	TTTGAGACCACCTGGCCAAACATGGCGAAATCACATCTCTACCAAAATTAACAAATAGCTGGGTGT GGTGTACATGCTATCGTAATCCAGCTACATCGGAGGCTGAGGCAGGAGAAATGCTTGAACCCA GGAGGCAGAGCTTGAGTGAGCCAAAGATCACACCCTGCACTTACAGCCTGGGTGACACAGTGGAGA CTCTGCTCAA
ESTD- D3S11	--	--	--	---	---	---	AACTGATTAGAACCTGAAATACATATTTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAAATAAGTACACTGTAATAAGAAATTAACAGAAATATCATTTGT TTATTCAAACTATTTATCATCTTATTTATGGTAAGCCATACTAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	---	AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCCAGGAGCCTTGATGTCATTCTGTATCTCCTCAG GTATCCCACTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTGTTAATTCAAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTGTC TGAGTCTTATCAAACTGACAGCCATTTATGCCACCTGAATATGGTCAGGTTACAGCTGTATCCC AGAAAGTGAACATACTGCTCTAGAACCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGCTCTTATTTGGAAGGATGCCGATGT
ESTD- D4S338	--	--	--	---	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGCGAGGTATGAAATGTATTT CTTAAACAATAAAGTTGAAAGTCCAAAATTTACTCCTTGATCCATGGACTGCAGAAATAAATGTTATTT TAGCTGTCAGAAAAACAATACTAATCTTGCAATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGTATT GCCAATAAGCAGTAATTTTGAGAGGAATCTTGTTTTCAATGCAAGTAG
ESTD- D4S95	--	--	--	---	---	---	CTTTCATGACGATAGGCTTCTCTACTAATACAGAAATTTTGAGAAGAGCAAAAACAACTTTCAAGG ATAATGGGCAATCACTTCTTCTTTCTTTAGAGTCTACCGG

ESTD-D7S399	--	--	--	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCTACATCATCTCTTTCACAAACATTTTCATCCATGGACTCCATACCTAG AATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DM	--	--	--	---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACAGTGGCTCAAGCAGCTGCTCGGCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGTGGGGAGGGAGACA GAATGCTGATTATCTGGTGAGAACCAAACTTCTGGCTGTGGTGGGAGGCTGCTTCCAAGACC TCCTGATTTGAGGAAGGGAGCAGCAGAGCGGAAGAGAACAGAGT
ESTD-DRD1	--	--	--	---	---	TCCCAGCCCTATCGGTATATTGGACTATGACACTGAGTCTCTCTGGAGAAAGATCCAAACCCATCAC ACAAAACGGTCAGCACCCCAACCTGAACCTCGCAGATGAATCTGCCACACATGCTCATCCCCAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAAAGAACTAAGGTAC
ESTD-DRD2	--	--	--	---	---	TCTGCTTTGGTGACGAGGCTGCCGGGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCGGTACAGCCCCATCCACCCAGCCACACAGCTGACTCTCCCGACCCG TCCACACAGGTCTCCACAGCACTCCGACAGCCCCGCAACCCAGAGAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD-DRD3	--	--	--	---	---	AAGACGATGGCCAGGATGAGCGGCAGTAGGAGAGGCGCATAGTAGGCTGTTGGGGGGCTGGCTGG CACCTGTGGAGTTCTCTGCCCAAGGTGTAGTTACAGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGGTGCGTATGCCAAGGGCTTCTGTGAGGAGA
ESTD-ERB82	--	--	--	---	---	TCTTTCAGGATCCGCATCTCGGCTGTTGGGCATCGCTCCGCTAGTGTACGCGCTCCACAGCTGG GGTGAGGGGGTGTGGGTGAGTCCGGGGCGGTGAGACCCACCGCGGCTGGAGGACTTCAACC CGCCTCACCTCCGTTTCTCGCAGCAGTCTCCGCATCGTGTACT
ESTD-ETS2	--	--	--	---	---	ACTCACAGTGTCTTTAAGTGAATGGTCGAGAAAGAGGCAACAGGAAGCCGTCCTGGCGCTGGCA GTCCGTGGGACGGGATGGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGTCTGGACACAC AGACTATTTTAGATTTCTTTTGCCTTTTGCACCAAGCAAGCAAAATGCAAAAACCTCTTTGAGAGG GTAGGAGGTGGGAAGGAACAACCATGTCTTTCAGAAAGTTAGTTG
ESTD-F2	--	--	--	---	---	GATAAGTACACTGAGGCCCCAGGAGGTATTGCCTAGTAGCCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCCCTCCAGGCCCGTAGGGGAACCTGGGGGATCTAGGGATGGGTGAGGAATGGCCC AGCCAGTCCCGCGGTGCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGGAGAGGATGGGC TGGATGAG
ESTD-F9	--	--	--	---	---	AGATCCTGATGATTTTTTCTATTTTTCTAAATGTTTTACAGTTTTGAAGTTTTAGATTTATGCCA TGCTCCATTTGAGTTAATATTGTGTAAAGTATGATGTTAAGTCAAACCTTCATTTTTTTTCCATA GGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAAAAAAC

ESTD- GODH	--	--	--	---	---	CGCAGACCGGTGAGTGTGGGTGGGAGTGTGAGGGAAGGAGGAGGAACCTGGGGTTTAGGGACT TTCCGGGTGACTTCCCGTTCTGTGCTTGCAGAGAAAGCGGGGAGAACACAGAGCCAACTGGCTAA GTGTAAGGAGCTCTGTGTCGACCGTGTGTCTGCTGCCCTGTTACGCTGTCTGTCTGCGCGCAGTCGA CTCTGTCCCGGAAATCCGAGAGCT
ESTD-GCK	--	--	--	---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTACGCCCTGCTGAGGCCACTCCTGGTCAACCATGAC AACCACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGATCCOACACCCACACCTGGCTGG AGCAGGAAATGCCGAGCGGCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCACC TGCAGCCTAATTACTCAAAGCTGTCCCAGGTCACAG
ESTD- GNAT2	--	--	--	---	---	GACCCTGAGTACCTOCTAGTGAGCAAGATGTCTCCGATCCAGGGTCAAAACACACAGGCATCATTG AAACCAAGTTTTCCGTCAAAGACTTGAATTCAGGTAAGTGCATGGTTCCTTAGG
ESTD- GPPK2L	--	--	--	---	---	AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTACCGCGGAGAACTGCTCGATATC
ESTD- HPRAS	--	--	--	---	---	CTGGGCTCGCCGACAGCAGCTGCTGGCACCTGGACGGCGGCCAGGCTCAOCTCTATAGTGGGTGCG TATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	--	---	---	TTGAAAGTTTCCACTGTTAACCAGTCTATGTTGGCAATGTGGCCTGGGCCCCACATTCTGGCCTTG AGGGCCTGCAGGACCCCAAGAGGCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCTCACCAAAGCTATGATAACCTTAATACCCCTGAGCAAGAGTTCGGCCTCCGGCTTGATTCC AGATGGAGCTTCCCTTATCCCTGATGATGATGGATTGGCTTCTCTGCTG
ESTD-HT2	--	--	--	---	---	GGGCTAAAAATTTCCGAGCAACTTTCATAGACTGTTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGGAGAGGAAGATGTGTACAGTTTGTGAGAGAGATAAAAGGATAACCTGGGTTTTCTGTGC TTTGCTTCTTCACATCCCTGGGAGTTAATAGCTGCAATTTTTCAAAGAACGGTATACAGGGACAGCA AAGCGAGTCGTGAAGTTTTCAAACAAGACACACCTT
ESTD-HT4	--	--	--	---	---	ACCAACGAGCCGGATACAGACACTCTTAAGTTTTGCCCTAAGGCTCATCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGTGCTTCTATCGGCAAGATGCGTACTTATTTGAATAGTAGAGGTAA ACACACGCCCCCAAGAGTCACTGAGACTGGCAGCTTCTGCAGCAGGCGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGGCGCCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	---	---	AACACACAAGCCCCAGCGAGAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTGTCTAACCCCT GAGCTATGAGCCCTCGTCTGCTGTGGTTTTCTTCTCTTCACTTATAGATTGATGTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTAGCTTGAGTAAAAATCCAGGATATTCTCCTACAAAATGAAA ACATTTTCGTCTGTAAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	--	--	---	---	ACCCAGTGGAGCCCGCTCATTTGCACGGTCTTGGCAGGAGGTGCCCTGGGAGAGAAGGAAGATGTTT CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-6	--	--	--	---	---	TTTACTATTCAATGGATACAGAAATTGTGGGAGTCACTATATCTCTATGAACAAAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCTACATGTTGAGTGACGGGAGTGGTGATCCGAGAGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGAAAGATGAGTATCTATGATACGAACGTAAAGT ATGTAAATACTTCACAAAATACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	--	---	---	CAAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATATTATTATTATTATTATTTTGG AGATGGAGTCTGGCTCTGTCACCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCCTCTGGGTTTCATGCCATTCTCGCTCAGCTCCGAGTCCGAGTAGCTGGGAATACAGGCACCCGCCACT GTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTTCAACCGT
ESTD-IL1B	--	--	--	---	---	CCACTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTTATGAGGGTGT GGGTCTCTACCTTGGGTGCTCTCTGCTCAGGAGCTCTCTGTCATTTGCAGG
ESTD- KRT10	--	--	--	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTAAAGTAAGTCTGCTAAGGTTTTTCCATTAAACCACTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGAGTGTGCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTAACCAGTATTGATA
ESTD- KRT8	--	--	--	---	---	ACCCTACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCTCAAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCACGTCACATTTGACACA
ESTD- LF79	--	--	--	---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAAATTTGAACCGTAGCAAAACTGCATTGGTATTAGA AAATAAAAATTTCCAATATGATGCTGTGTATACCTCTGCCTGCCATGCAGCATCATAGCCTGT GGGAACCGAGGGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	---	---	TACACACTTCTTACCCATTCACTGAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	--	---	---	TGTCAGTGTCCCTAGGGGCACCTCACCACCTCCAGCTTCTCAGCTGTGCTGCTGCTGCTGCTGCA AGGGTTTGTCTTAATCTCAATCAATGCTCTCTCATCTTTAGCAGCTGTGGGTTTTTGTGTTGTTT TCTGTTTTTGTCTAGTATCTGACTACTTTTTAATTATAAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAAGTTCACAACATTTAATAAAATTTTTCACCTG
ESTD-MCC	--	--	--	---	---	TTGTCAGGAGTGTGCTGATGCTGCCCTCCAGCTCTGCTCCTAGCCGAACITCAGGACAACGTGCAG CATCCATGTAGGAGAGCCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGATCCCCGAA TCTCAGGAAGTCTGCTCTTCCAAAGGGTTTGGTCTAAGTGTGCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGTTCTGTTTGTGTTTGTGATGG
ESTD-NF1	--	--	--	---	---	ATTATCCAGATGAATTTACAAAACATATACCAGATCCACAGACTGATATGGCTGGT

ESTD- NFKB1	--	--	---	---	---	AACATGGACTTGATATTTGTACAAAAAAGTTTTATTTCTAAAAAAGAAAAAAGAGAAA AAATTTAAGGGTGACTTATATCCACACTGCACACTGCGTAGCCCAAAACGCTTATTGTGGTAGG ATCAGCCCTCATTTTGTGCTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTGAAATCTGAG AAACTCTTTTAAACCTCACCTTTGTGGGTTTTTGGAGAAAGGTTATCA
ESTD- NPPA	--	--	---	---	---	TGTCCTAGGCCACGCCCTGCTTGCTCCCTGGCTGTTATCTTCAGTACTGCAAGAGAACACACAGAC AT
ESTD- NRAMP	--	--	---	---	---	GGAGGCAGGAGGTGGGAGGGGTCTGCTGCTCCAGGTCCACAGACCCAGAGAGGGCGCTCAGTG TATCCACACCCCAATGTGGCGCTGGGAGATGAAGAGGAGTTGATGACGGT
ESTD- NPRAS	--	--	---	---	---	GTGTTTTCTTAATCTTTCCAGGAACACAGTGACCATAATTTCTTTCTGCAGGCATATAGAAATTTGGT GGGTTTTCTTTATGTAGGGTGATATTGGATACTTTTTTGTGTGATTATATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTATGCTTATTTAACCTTGGCAATAGCATTCG ATCCCTGTGGTTTTTAATAAAAAAT
ESTD-OTC	--	--	---	---	---	GTGACCTTCTACCTTTAAAAAACTTTACCGGAGAAGAAATTAATATATATGCTATGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGGAGAGGTATGTAACA
ESTD-PAI1	--	--	---	---	---	GCCACCAACCAACCCACCCAGCACACCTCCAACTCCAGCAGACAAGTTGTTGACACAAGAGAGCC TCAGGGCACAGAGAGAGTCTGGACACGTGGGAGTGACCGCTGTATCATCGGAGCGCGCGGCAC ATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGCCCCAAGTCTAGACAGACAAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	--	--	---	---	---	CTCTTCAGGAACCAACCACTTCTTACCAACACGACTTATTGCTGCCGAGAGGTACAAACCCGTAGA ACTCTTCTTAACGTAAATTTAGTTAAAGGAATCGAAACCTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTCATTAGCTCTGTGAGTGTCTTCTTCTCACTTTCTGTGTTCTAGAACGTTTCTAG GACTGGCAGTTAAGCTTTCACCTAGGCTTCTGTATACCCATGCC
ESTD- PBDA	--	--	---	---	---	CCTTCTATGCCAGATGGAATTCAGTCCCTTCAGGATCGCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCAGGACTAATCCAAATCTACCCGAGCTTGCTCGCATACAGACG GACAGTGTGGTGGCAACATTGAAGCCCTGTACC
ESTD-PS-1	--	--	---	---	---	GGGGAGTAAACTTGGATTGGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCCTCAGCAACA GCCAGTGGAGACTGGAACACCAACCATAGCCTATTTCGTAGCCATATTAATGGTTGTGCCCTTACATT ATTACTCTTGCCATTTTCAAGAAAGCAATTGCCAGCTCTCCAAATCTCCATCACCTTTGGGGCTTGTTTT CTACTTGGCACAGATTATCTTGA
ESTD- PXMP1	--	--	---	---	---	ATGAACATGTTCTTTAATTTATGATATGTTTATAGTATCTTAAAAAGGCTCTTTTTTTTTTA ATGCAGAAAGAGGGGAAAAAAGAGCGAGCTGTGGTGGACAAGGTGTTTTCTCAAGGCTCATACAGA TTCTGAAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAAAGTCTTATGAAATTTAATCTT
ESTD- Per/IRDS	--	--	---	---	---	ACCTACAGACGTGCTGGATGGTGTGTCCAAACCCGAGGAATCTGAGAGCGAGCAGGGCTGGCTG CTGGAGAAAGAGCGTGGCGGAGACCTGGAAGGCT

ESTD-PDS	--	--	--	---	---	CCCGAGGAATCTGAGAGCGAGAGCGAGGGCTGGCTGTGGAGAAGAGCGTGCCGGAGACCTGGAAGG CCTTCTGGAGAGTGAAGAAGCTGGCAAGGGCAACAGTGGAGCCGAGGGCGCAGACGCAGG CCAGCCCCAGAGCGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCAACACTGAGAAATAGTGCAC CCAAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- RYR1	--	--	--	---	---	CTTCGTGACGGAGGTACGCTCTCCGCTCTTTCATGGACATATGGATGAGTGTGACCATTTCCC CTGCTGACAGTATGACAGCGAGACTTGTCTACTATGAGAGGGGAGCTGTGTGACATCATGCCCGC TCCCTCTGGAGGCTGGAGCCACTGAGAAATCAGCTGAGTGGAGGCCACCTGCCCTGGGGCCAGCCACT CCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	---	---	TGAACACCCCTGTGTCGGAGCCAGGTTGTGTTCTCCTGGGAGCCTGAGGAGTTTGTGTGTGTG CAGTCCCCCGGCCACTGCTGTTGAGCCTGGACATACACCTTCACCTCCTTTGGCCCGGAGAAAGAC ATTTACCCACTGGCCATGTCCTGGCTGTTGTGCACACCCCTCTGTGAAGACCCCAACCCCTGCCTCC CCACCCAAAGCCAGTTTCCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	---	---	TTCACTTTGTGGATTGTTCTTTTGTGTGCAGCACCTTTCAACATGATGTATCCCATTTGTCCAAG TTTGCTTTGGCTGCCCTGTGCTGTGGGATATTTGAAAGAGATCTTTGCCAGTCCAATGTCTAGAGAG TTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTAGATTTAAGTCTTAAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	--	--	--	---	---	AAATGGTCAGGACCCTGATCCACAAGAAAGTGTGACCATTTTCATCAGGGCCATCAGTTTCATCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTCAATCATCTTAAATGACTTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTACAACTTTCTCCAGTATGGATGGATTATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCCATGAGACACATCA
ESTD- THR8	--	--	--	---	---	TGCGGCTTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTGATTTCCAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATCACTTCATCCA CACTGGATTGGCCAAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	TTCTGTCATCCTGTCTGGAAGTTAGAAGGAAACAGACCAGACCTGGTCCCCCAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTTCAGCCTCCAGGCTCTACACACAAATCAGTCAGTG GCCAGAAAGACCCCCCTCAGAAATCGGAGCAGGGAGGATGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCTCCAACTTTCCAAATCCCGGCCCGCGATGG
ESTD-TYR	--	--	--	---	---	TAGTGAAGTTTTCATCTCCTGTGAGCTTCTGGATTCTTGTTCACCCGCAACAAGAGTCTATGC CAAGCGAGAAAGCTGGTCTCATGGGCAAAATCAATGTCTCTCCAGATTCAGATCCCCCAAGCA GTGCATCCATTGACACATAATATGCAATCCAGACAAGAGGTCATAAATATTGATGTGCTTAAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCTATGGGGATGACA

ESTD- TYRP1	--	--	---	---	---	AGTAGTGGATGAAGCTAACCCAGCCTCTCCTCACTGATCAGTATCAATGCTGAAGAATATGAA AACTCCAGAATCCTAATCAGTCTGGTCTAACAAATGCCCTACTCTCTTATGCAATTAGTATCACAA AACCACCTGGTTGAATATAATAGATTGAGTTATTAACTGATTTTCTTTCACCTTATTACCTCTCTTCT AATACAAGCATATGTTAGAAATTAAAGTTCTAGGCATACIT
ESTD- VB12	--	--	---	---	---	TTCCAAAGGCTCAATACAAGTCTTTTCTTGGATTACAACATCAGGGTCTGTTGTTTCTATTACA GGACACATGGATGCTGGAAATCACCCAGAGCCCAAGACACAAGGTACAGAGACAGGAACACCCAGTG ACTGTAGATGTCACCAGACTGAGAACCCACCGTTATATGTAAGTATCGATCGACAAGACCCGGGCGATG GGCTGAGGCTGATCCATTACTCATAT
ESTD-VWF	--	--	---	---	---	AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCCTTTGG TCCCTAGAGTCTG
ESTD-WT1	--	--	---	---	---	AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCGCTGCAGGATGTG CGACGTGTGCTGGAGTAGCCCGACTCTTGACGGTGGCATCTGAGACCCAGTGAGAAACGCCCTT CATGTGTGCTTACCCAGGCTGCAA
ESTD- s14544	--	--	---	---	---	TTGGGAAGTTAGAGCCTATATTAAATACGGAATTAAGGCAGGACACAGAGGCTTAATTGA TATCCCAAAGTTGAAATGTCTCAGTTCCGCTGTGTGGGTTAGATGCAGGATTTATATGATCCGTTAACCC TCT
EST71770	--	--	---	---	---	AGCACCACTCTCACGTCAAGCCTCAGCACCAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCTCCATGAAGAGCACAGAGAGTTATTTATCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTAAGTGTGATTGTGAACAACAAGAGAAACCACTGCAGAGTACCAGCTGTTGGTGGAAAGG AGTGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAAG
EST52418	--	--	---	---	---	CAAAATACAGGGTCAACTGCTATGATGTGTTGGAGCCAGTCAACCTTTGTTGGCTACAAGATGTG GGGAGTGGCCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAAAGTGAACCTGTGAGTGTGG CCCACCTGATTTGCCAGCCCGGACAGAGCTGATCCTTGAAGTCTTAAGTTCCACATGGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTGCTTATCAGCCTCCAGCCACAGCCCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAAGGAGGTGCGTCTGCTGCTGCCCG GTCACTC
EST13586	--	--	---	---	---	AGGCAGAAACTGGGGCCCCCATGCGGGGGGACGTGGAAGGCCACTTGAGCTTCTCTGGAGAGGACCTGA GGGACAAGGTCAACTCCTTCTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAAGACTCTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGGAGGAGGAGGATGCTGCGGCC CCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST51976	--	--	---	---	---	

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EST11458 6	--	--	--	---	---	CCACTTTGGTAGTGCCAGTGACTCATCCACAATGATTTCTCCAGTGCTCATCTTGTTCTCGAGTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCCAAAGCCAGATGATTTACCATTTTCCACAGTGGT CCCATTAATAAACATTCTATGAGCCAGGAGAGATACGTAATCTCGAAGCCGGCTATGTGTCC CGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	--	---	---	CGGTCTCCTCCAGGTATTGTTGCAGAAGCCGAGATGACCTCTATGCTCAGATGCATTCCATAAG GCATTTCTGAGGTAGTACACCTTCCCCACTCTTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACAGTGGAAAGGCCTGTTCCAGTGTTAAGGCATGCAAAAGGCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	--	--	--	---	---	ACCTGGTGTGCTGGTGTGGGTGAACCTGGTCTCTTGCCATTGCCGGCCCTCTCTGGGCCCGGTGG TCTCTCTGGTGTGGGTAGTCTGGAGTCAACGGTGTCTCTAGTGAAGCTGGTCTGATGGCAACC CTGGGAACGATGTTCCCTCCAGGTGCGGATGTTCAACCGGACACAAGGAGAGCGCGGTTACCCCTGG CAATAT
EST36027 2	--	--	--	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCTGCTGGCCAACTATGCTCTCAGA ACATCACTACCTACCTGCAAGAACAGCATTGCATACATGGATGAGGAGACTGGAAACCTGAAAAAGG CTGTCACTTACAGGGCTCTAATGATGTTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTTGTAGTGGTGTCTAAAAAGACAAATGAATGGGAAAGACAA
EST12274 0	--	--	--	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTCTTGCTTCCAATAGAGCCCTACCAAGTGTAT TACATAAAGAAAGTCAAGTGGTTTACTCTCATGACCAATATCTTCCCTCCTTAGGATGAGGTGA TAGTAAATGACCGATGGGTGAGAACTGTTCTGTCACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 EST44438 7	--	--	--	---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCGATTGTCTCTCCAGGGCCCTGTCTATC CAGTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCACTGCCCCCT GCTGCCATGTGGACTGGTCAAGTTGAGGACTTCTTG GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGACGTCCT GCTCCGACCTAAGCGGAGCAGCCCTCAAGAGCCGAGCGAGGTGGG
EST12839 3	--	--	--	---	---	TGCAAAACACACAAAAATCTTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTCTTGTCT CCTAACATCTATGTACTGGATTATCTAAATGAAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGGTGAATGATTCTGAGTAAGGAACTTGAATGTTATTCAACTGG ATTTCCAGTAGGTTTCACTTACTTATGAATATTATGATACTTAGCTTAG
EST54419 8	--	--	--	---	---	CTTCTGCCTAATTGAATGATATTGTTGCTGTGGGACCTGAGCACCTTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTTGGGTTAGCGTGGTCTGATGTTGCTACTA TAGTCCAAAGTGAA

EST26021 1	--	--	--	---	---	TAATGTAAGCTCATCCACCAAGAGCCTGCACCATGTTTTGAGGTTGAGTGACATGTTCCGAAACCTGT CCATAAAGTAATTTGTGAAAGAGGAGCAAGAGAACATTCTCTGCAGCACTTCACCTACCAAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGAGACTGAACCGACTTTTCTAAAGC TCTGAACAAAGCTTTCTTCTTTGCAACAAGACAAAGCAAGGCC
EST51212 0	--	--	--	---	---	ATCCTGAGCTCGCAATAAGCTTCTTGGTTCTACTTCTCTCCACAAGCCCAATTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCTTTGTGCTCCACTCAATACAAAAAGGCCCTCTCT ACATCT
EST20118 2	--	--	--	---	---	GTTCGAAATCCTCCTCTGAAAGTGGCCGGTTTAATCTGCTCATGACGCTGCGGCTGIGGTCAGCT GAGGTGAGGGCCCTTGAAGCTGGGAGTGGGTTTAGGACGCGGCTCTCTGCGTGCATCCTAAGCTCT GAGAGCAACCTCCCTTGAAGCTGGGAGTGGGTTTAGGACGCGGCTCTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	--	--	--	---	---	ACAATCAGGTCACACATTCCAGAAGAGGAGGGTGGTCAAGTGGCTGGGTAGGTCAGTAATCCA AGGATTCAGGAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	--	--	--	---	---	CTTCCTATGGGATTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGAGCTCATGACAATTTGAAGCTGACAATTACACAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTGAACCTTGGTGTACCTTTAATTACAACCTAG CAGACGGAAGTGAAGTCAAGGTAAGAAT
EST34088 2	--	--	--	---	---	GTGGGGCAACAGTGGGAGAGAGGGGGCCAGGGTATAAAGGGGGCCCAAGAGACCGGCTCAAGG ATCCCAAGGGCCCAACTCCCGAACCACTCAGGGTCTCTGTGACAGCTCACCTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	--	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCCACCCCTCTTCTCTTCCCTTGGGA CTTTGAGTCAAAATTGGCCTGACTTGAGTCCCTGAACCAAGCAAGAGAAAGAGGACCCCAAGAAAT CACAGGTGGCACGTCGGCTTACCGCCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT
EST74082	--	--	--	---	---	TCAGGGTGGCTGGACCCCAAGCCCAAGCTCTGCAGCAGGGAGGACGTGGCTGGGCTGCTGAAGCATG TGGGGTGAGCCCAAGGGCCCAAGGCAGGCACTGGCTTTCAGCTGCTCAGCCCTGCTGCTGCTC CCAGTCACTGCTCTTCTGCCATGGCCCTGTGGATGGCTCTCTGCCCTGCTGGCGCTGCTGGCCCTC TGGGGACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGGG
EST45311 0	--	--	--	---	---	GGCCTCCTCTCTTCCAAATCTGTCCCTATAGTTTCCCTATTAAGTGAACATGACATCTTTTAGT GGATAGATGCACACAAACACAAAGCCATTATGGGAAGGATCCACGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTTCATTTAACAGCCCTTATTCAATGGCCCTTTTCTTTTTCAGTAGTA CATACACATCTGTGTCATTGTGAAT

EST65258 8							TGCCCCATCAGCGCGGAGACATGGCTTGCCACAGCTCTTGAGATGTCACCAATTAACCCAGAAAT CCAGTTATTTCCACCTCAAAATGACAGCCATGGCGCGGGTCTTCTGGGGCTCGTCGGGGG ACAGCTCCACTCTGACTGGCAGCTTTGTCATGGAGACTTGAGGAGGGAGGCTTGAGGTTGGTGAG GTTAGTGCGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAAA
EST38216 3							ATGAGGATGAAGGTGGACAGGGAGGAGAGGGCCAACTGTGATCCAGGGCCTGCAGATGTCGCTG GACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782							ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCATTTGTTTAGCATTAACCTAA TTTTTTCCTGCTCCATGCAGACTGTAGCTTTACCTTAATGCTTATTTAAATGACAGTGGAAG TTTTTTTCCCTCGAAGTCCAGTATCCAGAGTTTGGTTTTTGAAC TAGCAATGCCTGTGAAAAA GAACTGAATACCTAAGATTCTGTCTTGGGTTTTTGTGTCATGCA
EST35879 9							GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCGTCCACCGATG GAACTGCCGGCAATCCTGACACGTGTGCACCGCTGTACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCGAAGACAGACGCGGATGGGGCAGGAGAGCTGCCTGGATGAA
EST68308 5							GGAAAGAGATTAAAGAGCTTGATTTGGACAATCTGGTTCTTTGAGTGTGGAAGATTTCATGCTCT GCCTGAGTTACAAACAGAACTCTTAGTACAGCGAGTAATAGATATATTGACACAGATGGGAATGGA GAAGTAGACTTTAAAGTAAGAAAGTAGTATTTTTTA
EST54045 6							GGAAATTTAAAAATATTTAAATACCTCCATTTTGCCTTATCCTTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAAGTTATGATTGTCATGTTGGCAATTTGTTTCTTACAAAATCGGATGGGAAATCT GTTAAGTAAGTACTGTTTGGCCTTGGAAATGGATTTTAAATGTGACTTTATCAT
EST52908 0							ATCACAGTCTCTGGTCTCTGGCCATCATTTCTTGGGAGAGATGGATGGTGTGCAAGCCCTTTGG CAATGTGAGATTGTATG
EST19590							AGGAGAAGCTGAGGAGGGGAAGAGAGACAGAATGACATTGATGAGTGAAGATGTCGGCTCAGGAT GCCGGAATGAC
EST76136							TGAAGCTTCTGCCAGCTTGCAATTGTTTCTAGGAGAACCCCGGTCATACCTTTATCTATAGCCTTCCCC TAGGTCTT
EST58607 0							CTCTGGATGGGTTACAGGTGGCAGGCACAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCTCTACATGGAGAACAGGACAGCCACATGGCGGGATGGCCGGCGGAGTTCTGGT TGCGGCCACGGCTGTGGCTCTGTTGTGAACGGTAGCCTTTGGGTTGCGATGCCTAAACCTTTGTTCT TGCCCAAGGAGGGCGGGTGCCATGCCTGAGATGTAGATGCGGCC
							Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence

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EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,
or a portion thereof which includes a polymorphic site,
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is
biallelic.
8. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is the reference base
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form
occupying the polymorphic site is an alternative form
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a
20 segment of a fragment shown in the Table, column 7 or
its complement.
11. The allele-specific oligonucleotide of claim 10 that is
a probe.

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12. The allele-specific oligonucleotide of claim 10,
wherein a central position of the probe aligns with the
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is
5 a primer.
14. The allele-specific oligonucleotide of claim 13,
wherein the 3' end of the primer aligns with the
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which
10 is selected from the group consisting of the nucleotide
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which
is selected from the group consisting of the nucleotide
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the
Table, column 7 or the complement thereof, wherein the
polymorphic site within the sequence or complement is
occupied by a base other than the reference base shown
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising
obtaining the nucleic acid from an individual; and
determining a base occupying any one of the polymorphic
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining
comprises determining a set of bases occupying a set of
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
- 5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.